

Sequence Listing

<110> Baker, Kevin P.  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Fong, Sherman  
Gao, Wei-Qiang  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth J.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Smith, Victoria  
Stewart, Timothy A.  
Tumas, Daniel  
Watanabe, Colin K.  
Williams, P. Mickey  
Wood, William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

<130> P2830P1C42

<150> 09/946374

<151> 2001-09-04

<150> 60/098716

<151> 1998-09-01

<150> 60/098723

<151> 1998-09-01

<150> 60/098749

<151> 1998-09-01

<150> 60/098750

<151> 1998-09-01

<150> 60/098803

<151> 1998-09-02

<150> 60/098821

<151> 1998-09-02

<150> 60/098843

<151> 1998-09-02

<150> 60/099536

<151> 1998-09-09

<150> 60/099596

<151> 1998-09-09

<150> 60/099598  
<151> 1998-09-09

<150> 60/099602  
<151> 1998-09-09

<150> 60/099642  
<151> 1998-09-09

<150> 60/099741  
<151> 1998-09-10

<150> 60/099754  
<151> 1998-09-10

<150> 60/099763  
<151> 1998-09-10

<150> 60/099792  
<151> 1998-09-10

<150> 60/099808  
<151> 1998-09-10

<150> 60/099812  
<151> 1998-09-10

<150> 60/099815  
<151> 1998-09-10

<150> 60/099816  
<151> 1998-09-10

<150> 60/100385  
<151> 1998-09-15

<150> 60/100388  
<151> 1998-09-15

<150> 60/100390  
<151> 1998-09-15

<150> 60/100584  
<151> 1998-09-16

<150> 60/100627  
<151> 1998-09-16

<150> 60/100661  
<151> 1998-09-16

<150> 60/100662  
<151> 1998-09-16

<150> 60/100664  
<151> 1998-09-16

<150> 60/100683

<151> 1998-09-17

<150> 60/100684  
<151> 1998-09-17

<150> 60/100710  
<151> 1998-09-17

<150> 60/100711  
<151> 1998-09-17

<150> 60/100848  
<151> 1998-09-18

<150> 60/100849  
<151> 1998-09-18

<150> 60/100919  
<151> 1998-09-17

<150> 60/100930  
<151> 1998-09-17

      <150> 60/101014  
      <151> 1998-09-18

      <150> 60/101068  
      <151> 1998-09-18

      <150> 60/101071  
      <151> 1998-09-18

      <150> 60/101279  
      <151> 1998-09-22

      <150> 60/101471  
      <151> 1998-09-23

      <150> 60/101472  
      <151> 1998-09-23

      <150> 60/101474  
      <151> 1998-09-23

      <150> 60/101475  
      <151> 1998-09-23

      <150> 60/101476  
      <151> 1998-09-23

      <150> 60/101477  
      <151> 1998-09-23

      <150> 60/101479  
      <151> 1998-09-23

      <150> 60/101738  
      <151> 1998-09-24

<150> 60/101741  
<151> 1998-09-24

<150> 60/101743  
<151> 1998-09-24

<150> 60/101915  
<151> 1998-09-24

<150> 60/101916  
<151> 1998-09-24

<150> 60/102207  
<151> 1998-09-29

<150> 60/102240  
<151> 1998-09-29

<150> 60/102307  
<151> 1998-09-29

<150> 60/102330  
<151> 1998-09-29

<150> 60/102331  
<151> 1998-09-29

<150> 60/102484  
<151> 1998-09-30

<150> 60/102487  
<151> 1998-09-30

<150> 60/102570  
<151> 1998-09-30

<150> 60/102571  
<151> 1998-09-30

<150> 60/102684  
<151> 1998-10-01

<150> 60/102687  
<151> 1998-10-01

<150> 60/102965  
<151> 1998-10-02

<150> 60/103258  
<151> 1998-10-06

<150> 60/103314  
<151> 1998-10-07

<150> 60/103315  
<151> 1998-10-07

<150> 60/103328

<151> 1998-10-07

<150> 60/103395  
<151> 1998-10-07

<150> 60/103396  
<151> 1998-10-07

<150> 60/103401  
<151> 1998-10-07

<150> 60/103449  
<151> 1998-10-06

<150> 60/103633  
<151> 1998-10-08

<150> 60/103678  
<151> 1998-10-08

<150> 60/103679  
<151> 1998-10-08

<150> 60/103711  
<151> 1998-10-08

<150> 60/104257  
<151> 1998-10-14

<150> 60/104987  
<151> 1998-10-20

<150> 60/105000  
<151> 1998-10-20

<150> 60/105002  
<151> 1998-10-20

<150> 60/105104  
<151> 1998-10-21

<150> 60/105169  
<151> 1998-10-22

<150> 60/105266  
<151> 1998-10-22

<150> 60/105693  
<151> 1998-10-26

<150> 60/105694  
<151> 1998-10-26

<150> 60/105807  
<151> 1998-10-27

<150> 60/105881  
<151> 1998-10-27

<150> 60/105882  
<151> 1998-10-27

<150> 60/106023  
<151> 1998-10-28

<150> 60/106029  
<151> 1998-10-28

<150> 60/106030  
<151> 1998-10-28

<150> 60/106032  
<151> 1998-10-28

<150> 60/106033  
<151> 1998-10-28

<150> 60/106062  
<151> 1998-10-27

<150> 60/106178  
<151> 1998-10-28

<150> 60/106248  
<151> 1998-10-29

<150> 60/106384  
<151> 1998-10-29

<150> 60/108500  
<151> 1998-10-29

<150> 60/106464  
<151> 1998-10-30

<150> 60/106856  
<151> 1998-11-03

<150> 60/106902  
<151> 1998-11-03

<150> 60/106905  
<151> 1998-11-03

<150> 60/106919  
<151> 1998-11-03

<150> 60/106932  
<151> 1998-11-03

<150> 60/106934  
<151> 1998-11-03

<150> 60/107783  
<151> 1998-11-10

<150> 60/108775

<151> 1998-11-17

<150> 60/108779  
<151> 1998-11-17

<150> 60/108787  
<151> 1998-11-17

<150> 60/108788  
<151> 1998-11-17

<150> 60/108801  
<151> 1998-11-17

<150> 60/108802  
<151> 1998-11-17

<150> 60/108806  
<151> 1998-11-17

<150> 60/108807  
<151> 1998-11-17

      <150> 60/108848  
      <151> 1998-11-18

      <150> 60/108849  
      <151> 1998-11-18

      <150> 60/108850  
      <151> 1998-11-18

      <150> 60/108851  
      <151> 1998-11-18

      <150> 60/108852  
      <151> 1998-11-18

      <150> 60/108858  
      <151> 1998-11-18

      <150> 60/108867  
      <151> 1998-11-17

      <150> 60/108904  
      <151> 1998-11-18

      <150> 60/108925  
      <151> 1998-11-17

      <150> 60/113296  
      <151> 1998-12-22

      <150> 60/114223  
      <151> 1998-12-30

      <150> 60/129674  
      <151> 1999-04-16

<150> 60/141037  
<151> 1999-06-23

<150> 60/144758  
<151> 1999-07-20

<150> 60/145698  
<151> 1999-07-26

<150> 60/162506  
<151> 1999-10-29

<150> 09/218517  
<151> 1998-12-22

<150> 09/284291  
<151> 1999-04-12

<150> 09/403297  
<151> 1999-10-18

<150> 09/872035  
<151> 2001-06-01

<150> 09/882636  
<151> 2001-06-14

<150> PCT/US99/00106  
<151> 1999-01-05

<150> PCT/US99/20111  
<151> 1999-09-01

<150> PCT/US99/21194  
<151> 1999-09-15

<150> PCT/US99/28313  
<151> 1999-11-30

<150> PCT/US99/28551  
<151> 1999-12-02

<150> PCT/US99/30095  
<151> 1999-12-16

<150> PCT/US00/00219  
<151> 2000-01-05

<150> PCT/US00/00376  
<151> 2000-01-06

<150> PCT/US00/03565  
<151> 2000-02-11

<150> PCT/US00/04342  
<151> 2000-02-18

<150> PCT/US00/05004

<151> 2000-02-24

<150> PCT/US00/05841  
<151> 2000-03-02

<150> PCT/US00/06884  
<151> 2000-03-15

<150> PCT/US00/13705  
<151> 2000-05-17

<150> PCT/US00/14042  
<151> 2000-05-22

<150> PCT/US00/14941  
<151> 2000-05-30

<150> PCT/US00/15264  
<151> 2000-06-02

<150> PCT/US00/23328  
<151> 2000-08-24

<150> PCT/US00/23522  
<151> 2000-08-23

<150> PCT/US00/30873  
<151> 2000-11-10

<150> PCT/US00/30952  
<151> 2000-11-08

<150> PCT/US00/32678  
<151> 2000-12-01

<150> PCT/US01/06520  
<151> 2001-02-28

<150> PCT/US01/06666  
<151> 2001-03-01

<150> PCT/US01/17800  
<151> 2001-06-01

<150> PCT/US01/19692  
<151> 2001-06-20

<150> PCT/US01/21066  
<151> 2001-06-29

<150> PCT/US01/21735  
<151> 2001-07-09

<160> 477

<210> 1  
<211> 43  
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Sequence - Artificial

<400> 1  
tgtaaaacga cggccagttt aatagacctg caattattaa tct 43

<210> 2

<211> 41

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-41

<223> Sequence - Artificial

<400> 2  
caggaaacag ctatgaccac ctgcacacacct gcaaattccat t 41

<210> 3

<211> 1110

<212> DNA

<213> Homo sapiens

<400> 3  
ccaatcgccc ggtgcgggtgg tgcagggtct cgggctagtc atggcgtccc 50  
cgtctcggag actgcagact aaaccagtca ttacttggtt caagagcgtt 100  
ctgctaattct acacttttat ttcttggatc actggcgtta tccttcttgc 150  
agttggcatt tggggcaagg tgagcctgga gaattacttt tctcttttaa 200  
atgagaaggc caccaatgtc cccttcgtgc tcattgtac tggtaccgtc 250  
attattcttt tgggcacctt tggttgtttt gctacctgcc gagttctgc 300  
atggatgcta aaactgtatg caatgtttct gactctcggtt tttttggtcg 350  
aactggtcgc tgccatcgta ggatttggttt tcagacatga gattaagaac 400  
agcttttaaga ataattatga gaaggctttg aagcagtata actctacagg 450  
agattataga agccatgcag tagacaagat ccaaaatacg ttgcattgtt 500  
gtgggtgtcac cgattataga gattggacag atactaatta ttactcagaa 550  
aaaggatttc ctaagagttg ctgtaaacctt gaagattgtt ctccacagag 600  
agatgcagac aaagtaaaca atgaaggttg ttttataaaag gtgtatgacca 650  
ttatagagtc agaaatggga gtcgttgcag gaatttcctt tggagttgtt 700  
tgcttccaac tgattggaat ctttctcgcc tactgccwct ctcgtgccat 750

aacaataac cagtagaga tagtgtaacc caatgtatct gtgggcctat 800  
tcctctcac cttaaggac attagggtc cccctgtga attagaaagt 850  
tgcttggctg gagaactgac aacactactt actgatacac 900  
caccaggtagg ttgattcaat caagatgtat gtagacctaa aactacacca 950  
ataggctgat tcaatcaaga tccgtgctcg cagtggctg attcaatcaa 1000  
gatgtatgtt tgctatgttc taagtccacc ttctatccca ttcatgttag 1050  
atcgttgaaa ccctgtatcc ctctgaaaca ctggaagagc tagtaaattt 1100  
taaatgaagt 1110

<210> 4  
<211> 245  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-42  
<223> Signal Peptide

<220>  
<221> TRANSMEM  
<222> 19-42, 61-83, 92-114, 209-230  
<223> Transmembrane Domains

<220>  
<221> misc\_feature  
<222> 69-80, 211-222  
<223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>  
<221> misc\_feature  
<222> 75-81, 78-84, 210-216, 214-220, 226-232  
<223> N-Myristoylation Site.

<220>  
<221> misc\_feature  
<222> 134-138  
<223> N-Glycosylation Site.

<220>  
<221> misc\_feature  
<222> 160-168, 160-169  
<223> Tyrosine Kinase Phosphorylation Site.

<220>  
<221> unsure  
<222> 233  
<223> unknown amino acid

<400> 4  
Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr

1	5	10	15											
Cys	Phe	Lys	Ser	Val	Leu	Leu	Ile	Tyr	Thr	Phe	Ile	Phe	Trp	Ile
				20				25					30	
Thr	Gly	Val	Ile	Leu	Leu	Ala	Val	Gly	Ile	Trp	Gly	Lys	Val	Ser
				35				40				45		
Leu	Glu	Asn	Tyr	Phe	Ser	Leu	Leu	Asn	Glu	Lys	Ala	Thr	Asn	Val
				50				55				60		
Pro	Phe	Val	Leu	Ile	Ala	Thr	Gly	Thr	Val	Ile	Ile	Leu	Leu	Gly
				65				70				75		
Thr	Phe	Gly	Cys	Phe	Ala	Thr	Cys	Arg	Ala	Ser	Ala	Trp	Met	Leu
				80				85				90		
Lys	Leu	Tyr	Ala	Met	Phe	Leu	Thr	Leu	Val	Phe	Leu	Val	Glu	Leu
				95				100				105		
Val	Ala	Ala	Ile	Val	Gly	Phe	Val	Phe	Arg	His	Glu	Ile	Lys	Asn
				110				115				120		
Ser	Phe	Lys	Asn	Asn	Tyr	Glu	Lys	Ala	Leu	Lys	Gln	Tyr	Asn	Ser
				125				130				135		
Thr	Gly	Asp	Tyr	Arg	Ser	His	Ala	Val	Asp	Lys	Ile	Gln	Asn	Thr
				140				145				150		
Leu	His	Cys	Cys	Gly	Val	Thr	Asp	Tyr	Arg	Asp	Trp	Thr	Asp	Thr
				155				160				165		
Asn	Tyr	Tyr	Ser	Glu	Lys	Gly	Phe	Pro	Lys	Ser	Cys	Cys	Lys	Leu
				170				175				180		
Glu	Asp	Cys	Thr	Pro	Gln	Arg	Asp	Ala	Asp	Lys	Val	Asn	Asn	Glu
				185				190				195		
Gly	Cys	Phe	Ile	Lys	Val	Met	Thr	Ile	Ile	Glu	Ser	Glu	Met	Gly
				200				205				210		
Val	Val	Ala	Gly	Ile	Ser	Phe	Gly	Val	Ala	Cys	Phe	Gln	Leu	Ile
				215				220				225		
Gly	Ile	Phe	Leu	Ala	Tyr	Cys	Xaa	Ser	Arg	Ala	Ile	Thr	Asn	Asn
				230				235				240		
Gln	Tyr	Glu	Ile	Val										
				245										

<210> 5

<211> 1218

<212> DNA

<213> Homo sapiens

<400> 5

cccacgcgtc cggcgccgtg gcctcgcgtc catcttgcc gttctctcg 50

acctgtcaca aaggagtcgc gccggccgccc cggccccctc cctccgggtgg 100  
gcccgagg tagagaaaagt cagtgccaca gcccgaccgc gctgctctga 150  
gccctggca cgccgaacgg gagggagtct gagggtttggg gacgtctgtg 200  
agggagggga acagccgctc gagcctgggg cgggcggacc ggactggggc 250  
cggggttaggc tctggaaagg gcccggaga gaggtggcgt tggtcagaac 300  
ctgagaaaaca gccgagaggt tttccaccga ggcccgccgt tgagggatct 350  
gaagaggttc ctagaagagg gtgttccctc tttcgggggt cctcaccaga 400  
agaggttctt ggggtcgcc cttctgagga ggctgcggct aacagggccc 450  
agaactgcca ttggatgtcc agaatcccct gtagttgata atgttggaa 500  
taagctctgc aactttcttt ggcattcagt tgtaaaaaac aaataggatg 550  
caaattccctc aactccaggt tatgaaaaca gtacttgaa aactgaaaac 600  
tacctaaatg atcgtctttg gttggccgt gttcttagcg agcagaagcc 650  
ttggccaggg tctgttgtt actctcgaag agcacatagc ccacttccta 700  
gggactggag gtgccgctac taccatgggt aattcctgtt tctgccgaga 750  
tgacagtggaa acagatgaca gtgttgacac ccaacagcaa cagggcggaa 800  
acagtgcagt acccactgct gacacaagga gccaaccacg ggaccctgtt 850  
cggccaccaa ggagggcccg aggacctcat gagccaagga gaaagaaaca 900  
aaatgtggat gggctagtgt tggacacact ggcagtaata cggaactttt 950  
tagataagta agtatctgac tcacggtcac ctccagtggaa atgaaaagtg 1000  
ttctgcccgg aaccatgact ttaggactcc ttcagttcct ttaggacata 1050  
ctcgccaagc cttgtgctca cagggcaaag gagaatattt taatgctccg 1100  
ctgatggcag agtaaatgat aagatttgat gtttttgctt gctgtcatct 1150  
actttgtctg gaaatgtcta aatgtttctg tagcagaaaa cacgataaaag 1200  
ctatgatctt tattagag 1218

<210> 6  
<211> 117  
<212> PRT  
<213> Homo sapiens  
  
<220>  
<221> sig\_peptide  
<222> 1-16  
<223> Signal Peptide

<220>  
 <221> misc\_feature  
 <222> 18-24, 32-38, 34-40, 35-41, 51-57  
 <223> N-Myristylation Site.

<220>  
 <221> misc\_feature  
 <222> 22-26, 50-54, 113-117  
 <223> Casein Kinase II Phosphorylation Site.

<400> 6  
 Met Ile Val Phe Gly Trp Ala Val Phe Leu Ala Ser Arg Ser Leu  
     1               5               10                       15  
 Gly Gln Gly Leu Leu Leu Thr Leu Glu Glu His Ile Ala His Phe  
     20                       25                               30  
 Leu Gly Thr Gly Gly Ala Ala Thr Thr Met Gly Asn Ser Cys Ile  
     35                       40                               45  
 Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln  
     50                       55                               60  
 Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser  
     65                       70                               75  
 Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro  
     80                       85                               90  
 His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val Leu  
     95                       100                               105  
 Asp Thr Leu Ala Val Ile Arg Thr Leu Val Asp Lys  
     110                       115

<210> 7  
 <211> 756  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
 ggcacgaggc gctgtccacc cggggcggt ggagttaggt accagattca 50  
 gcccatttgg cccccacgcc tctgttctcg gaatccgggt gctgcggatt 100  
 gaggtcccggt ttccttaacgg actgcaagat ggaggaaggc gggAACCTAG 150  
 gagggcctgat taagatggtc catctactgg tcttgtcagg tgcctggggc 200  
 atgcaaatgt gggtgacctt cggttcaggc ttccctgttt tccgaaggct 250  
 tccccgacat actttcggac tagtgcagag caaaactcttc cccttctact 300  
 tccacatctc catgggctgt gccttcatca acctctgcat ctggcttca 350  
 cagcatgctt gggctcagct cacattctgg gagggccagcc agctttacct 400  
 gctgttcctg agccttacgc tggccactgt caacgcccgc tggctgaaac 450

cccgaccac agctgccatg tggccctgc aaaccgtgga gaaggagcga 500  
ggcctgggtg gggaggtacc aggccac cagggtcccc atccctaccg 550  
ccagctgcga gagaaggacc ccaagtacag tgctctccgc cagaatttct 600  
tccgctacca tgggctgtcc tctttgca atctggctg cgtcctgagc 650  
aatgggctct gtctcgctgg ccttgccctg gaaataagga gcctcttagca 700  
tggccctgc atgctaataa atgcttcttc agaaatgaaa aaaaaaaaaa 750  
aaaaaaaa 756

<210> 8  
<211> 189  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-24  
<223> Signal Peptide

<220>  
<221> misc\_feature  
<222> 4-10, 5-11, 47-53, 170-176, 176-182  
<223> N-Myristoylation Site.

<220>  
<221> misc\_feature  
<222> 44-85  
<223> G-protein Coupled Receptors Proteins.

<220>  
<221> misc\_feature  
<222> 54-65  
<223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>  
<221> misc\_feature  
<222> 82-86  
<223> Casein Kinase II Phosphorylation Site.

<220>  
<221> TRANSMEM  
<222> 86-103, 60-75  
<223> Transmembrane Domain

<220>  
<221> misc\_feature  
<222> 144-151  
<223> Tyrosine Kinase Phosphorylation Site.

<400> 8  
Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His  
1 5 10 15

Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr  
                   20                     25                     30  
  
 Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr  
                   35                     40                     45  
  
 Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile  
                   50                     55                     60  
  
 Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln  
                   65                     70                     75  
  
 His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr  
                   80                     85                     90  
  
 Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp  
                   95                     100                    105  
  
 Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val  
                   110                    115                    120  
  
 Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln  
                   125                    130                    135  
  
 Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr  
                   140                    145                    150  
  
 Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser  
                   155                    160                    165  
  
 Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala  
                   170                    175                    180  
  
 Gly Leu Ala Leu Glu Ile Arg Ser Leu  
                   185

<210> 9  
 <211> 1508  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
 aattcagatt ttaagccat tctgcagtgg aatttcatga actagcaaga 50  
  
 ggacaccatc ttcttgtatt atacaagaaa ggagtgtacc tatcacacac 100  
  
 agggggaaaa atgctctttt gggtgctagg cctcctaatac ctctgtggtt 150  
  
 ttctgtggac tcgtaaagga aaactaaaga ttgaagacat cactgataag 200  
  
 tacatttta tcactggatg tgactcgggc tttggaaact tggcagccag 250  
  
 aactttgat aaaaaggat ttcatgtaat cgctgcctgt ctgactgaat 300  
  
 caggatcaac agctttaaag gcagaaacct cagagagact tcgtactgtg 350  
  
 cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtgggt 400

gaagaaccaa gttgggaga aaggtctctg gggctgatc aataatgctg 450  
gtttcccg cgtgctggct cccactgact ggctgacact agaggactac 500  
agagaaccta ttgaagtgaa cctgttgga ctcatcagt tgacactaaa 550  
tatgcttcct ttggtaaga aagctcaagg gagagttatt aatgtctcca 600  
gtttggagg tcgccttgc atcgttggag gggctatac tccatccaaa 650  
tatgcagtgg aaggttcaa tgacagctt agacggaca tgaaagctt 700  
tggtgtgcac gtctcatgca ttgaaccagg attgttcaaa acaaacttgg 750  
cagatccagt aaaggtaatt gaaaaaaaaac tcgccattt ggagcagctg 800  
tctccagaca tcaaacaaca atatggagaa gttacattt aaaaaagtct 850  
agacaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg 900  
tggtagagtg catggaccac gctctaaca gtctcttccc taagactcat 950  
tatgccgctg gaaaagatgc caaaattttc tggatacctc tgtctcacat 1000  
gccagcagct ttgcaagact tttttttt gaaacagaaa gcagagctgg 1050  
ctaatcccaa ggcagtgtga cttagtaac cacaaatgtc tcctccaggc 1100  
tatgaaattt ggcgatttca agaacacatc tcctttcaa cccatttcc 1150  
tatctgctcc aacctggact cattagatc gtgtttttt ggattgcaaa 1200  
aggaggtccc accatcgctg gtggatatccc agggtccctg ctcaagttt 1250  
cttgaaaag gagggtggaa atggtagatc acataggcaa gtccgtccct 1300  
gtattttaggc ttgcctgct tgggtgtatg taaggaaat tgaaagactt 1350  
gcccattcaa aatgatctt accgtggcct gccccatgct tatggtcccc 1400  
agcatttaca gtaacttgg aatgttaagt atcatctt atctaaatat 1450  
taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaa 1508

<210> 10  
<211> 319  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-17  
<223> Signal Peptide

<220>  
<221> misc\_feature

<222> 36-47, 108-113, 166-171, 198-203, 207-212  
<223> N-myristoylation Sites.

<220>  
<221> misc\_feature  
<222> 39-42  
<223> Glycosaminoglycan Attachment Site.

<220>  
<221> TRANSMEM  
<222> 136-152  
<223> Transmembrane Domain

<220>  
<221> misc\_feature  
<222> 161-163, 187-190 and 253-256  
<223> N-glycosylation Sites.

<400> 10  
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu  
1 5 10 15  
Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys  
20 25 30  
Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala  
35 40 45  
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys  
50 55 60  
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu  
65 70 75  
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val  
80 85 90  
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly  
95 100 105  
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala  
110 115 120  
Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu  
125 130 135  
Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro  
140 145 150  
Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val  
155 160 165  
Gly Gly Arg Leu Ala Ile Val Gly Gly Tyr Thr Pro Ser Lys  
170 175 180  
Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys  
185 190 195

Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys  
 200 205 210  
 Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala  
 215 220 225  
 Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu  
 230 235 240  
 Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser  
 245 250 255  
 Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His  
 260 265 270  
 Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys  
 275 280 285  
 Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala  
 290 295 300  
 Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn  
 305 310 315  
 Pro Lys Ala Val

<210> 11  
 <211> 2720  
 <212> DNA  
 <213> Homo sapines

<400> 11  
 gcgggctgtt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50  
 gagctctcggtt ttcctctcagg tcggacttcc tgacgcccggcc agtggggcggg 100  
 gccccttggg ccgtcgccac cactgttagtc atgtaccac cgcgcggcc 150  
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200  
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250  
 caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300  
 gctttctgt ggactccctct tctacatcaa cttggctgac cattggaaag 350  
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400  
 gggtaaaaac cagcaaatcc acccgcttta ccagctccctc agaaggcgga 450  
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500  
 acatccagcg gggaccaccc cacctgcaga ttagaccccc aagccaagac 550  
 ctgaaggatg ggacccagga ggaggccaca aaaaggcaag aagcccctgt 600  
 ggatccccgc cccgaaggag atcccgagag gacagtcatc agtggaggg 650

gagcggtgat cgagcctgag cagggcacccg agctcccttc aagaagagca 700  
gaagtgccca ccaagcctcc cctgccacccg gccaggacac agggcacacc 750  
agtgcacatcg aactatcgcc agaagggcgt gattgacgac ttccctgcatg 800  
catggaaagg ataccgcaag tttgcattggg gccatgacga gctgaaggct 850  
gtgtccaggt ccttcagtga gtggtttggc ctccgtctca cactgatcga 900  
cgcgctggac accatgtgga tcttgggtct gaggaaagaa tttgaggaag 950  
ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgac 1000  
aacctgtttg agagcacatcg ccgcattcctg gggggctcc tgagtgccta 1050  
ccacccgtct ggggacagcc tcttcctgag gaaagctgag gatttggaa 1100  
atccggctaat gcctgccttc agaacaccat ccaagattcc ttactcgat 1150  
gtgaacatcg gtactggagt tgcccacccg ccacggtgga cctccgacag 1200  
caactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250  
gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300  
cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350  
caatacccac agtggccctct tcacccaccc gggcgtattc acgctggcgc 1400  
ccagggccga cagctactat gagtacctgc tgaaggcgtg gatccaggc 1450  
gggaagcagg agacacagct gctgaaagac tacgtggaaag ccatcgaggg 1500  
tgtcagaacg cacctgctgc ggcactccga gcccagtaag ctcacctttg 1550  
tgggggagct tgcccacggc cgcttcagtg ccaagatgga ccacctggtg 1600  
tgcttcctgc cagggacgct ggctctggc gtctaccacg gcctgcccgc 1650  
cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700  
accggcagat ggagacgggg ctgagtcgg agatcgtgca cttcaacctt 1750  
taccccccagc cggggccgtcg ggacgtggag gtcaagccag cagacaggca 1800  
caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgcg 1850  
tcacagggga ccccaaatac caggactggg gctggagat tctgcagagc 1900  
ttcagccgat tcacacgggt cccctcggtt ggctattctt ccatcaacaa 1950  
tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000  
tcctggggga gacgctcaag tatctgttct tgctcttctc cgatgaccca 2050  
aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100

gcctatctgg acccctgcct agggtgatg gctgctggtg tggggacttc 2150  
gggtggcag aggcacccctg ctgggtctgt ggcatttcc aaggcccac 2200  
gtagcacccgg caaccgccaa gtggcccagg ctctgaactg gctctggct 2250  
cctcctcgtc tctgcttaa tcaggacacc gtgaggacaa gtgaggccgt 2300  
cagtcttgtt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350  
ttcctccaga agacacgaat catgactcac gattgctgaa gcctgagcag 2400  
gtctctgtgg gccgaccaga gggggcttc gaggtggtcc ctggtaactgg 2450  
ggtagccgag tggacagccc agggtgcagc tctgcccggg ctctgtgaagc 2500  
ctcagatgtc cccaatccaa gggctggag gggctgcgt gactccagag 2550  
gcctgaggct ccagggctgg ctctgggtt tacaagctgg actcaggat 2600  
cctcctggcc gccccgcagg gggcttgag ggctggacgg caagtccgtc 2650  
tagctcacgg gccccctccag tgaaatgggt ctttcggtg gagataaaag 2700  
ttgatttgct ctaaccgcaa 2720

<210> 12  
<211> 699  
<212> PRT  
<213> Homo sapiens

<220>  
<221> TRANSMEM  
<222> 21-40 and 84-105  
<223> Transmembrane Domain (type II)

<400> 12  
Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser  
1 5 10 15  
Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala  
20 25 30  
Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro  
35 40 45  
His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr  
50 55 60  
Asp Asn Ser Lys Ser Trp Arg Arg Ser Cys Trp Arg Lys Trp  
65 70 75  
Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu  
80 85 90  
Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala  
95 100 105

Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys
				110					115					120
Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val
				125					130					135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro
				140					145					150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro
				155					160					165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly
				170					175					180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro
				185					190					195
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly
				200					205					210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg
				215					220					225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln
				230					235					240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp
				245					250					255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly
				260					265					270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe
				275					280					285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile
				290					295					300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Ala	Arg	Lys	Trp	Val	Ser	
				305					310					315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu
				320					325					330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu
				335					340					345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn
				350					355					360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser
				365					370					375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr
				380					385					390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe

395	400	405
Arg Glu Leu Ser Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala		
410	415	420
Val Glu Lys Val Thr Gln His Ile His Gly Leu Ser Gly Lys Lys		
425	430	435
Asp Gly Leu Val Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe		
440	445	450
Thr His Leu Gly Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr		
455	460	465
Tyr Glu Tyr Leu Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu		
470	475	480
Thr Gln Leu Leu Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg		
485	490	495
Thr His Leu Leu Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val		
500	505	510
Gly Glu Leu Ala His Gly Arg Phe Ser Ala Lys Met Asp His Leu		
515	520	525
Val Cys Phe Leu Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly		
530	535	540
Leu Pro Ala Ser His Met Glu Leu Ala Gln Glu Leu Met Glu Thr		
545	550	555
Cys Tyr Gln Met Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu		
560	565	570
Ile Val His Phe Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val		
575	580	585
Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr		
590	595	600
Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys		
605	610	615
Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe		
620	625	630
Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln		
635	640	645
Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe		
650	655	660
Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp		
665	670	675
Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala		
680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala  
695

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.  
  
<400> 13  
cgccagaagg gcgtgattga cgtc 24

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 14  
ccatccttct tcccagacag gccg 24

<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 15  
gaagctgtg tccaggtcct tcagttagtg gtttggcctc ggtc 44

<210> 16  
<211> 1524  
<212> DNA  
<213> Homo sapiens

<400> 16  
ggcgccgcgt aggccccggaa ggccggggccg gccgggctgc gagcgctgc 50  
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gagaaaagcg 100  
gcgcagctgc cctgggagga cggcaggtcc gggtttgctct ccggcggcct 150  
ccctcggaag tggccgtct tccacctgtt cgtggcctgc ctctcgctgg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggcctc cccgtgcctg 300  
ccccccagag ccgccccctg agcactggga agaagacgca tcctgggcc 350  
cccaccgcct ggcagtgctg gtgccttcc gcgaacgctt cgaggagctc 400  
ctggtcttcg tgccccacat gcgcgccttc ctgagcagga agaagatccg 450  
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500  
cagcgctcat caacgtggc ttcctggaga gcagcaacag cacggactac 550  
attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600  
tggcttcct gaggctggc cttccacgt gcctccccc gagctccacc 650  
ctctctacca ctacaagacc tatgtcggcg gcacccctgct gctctccaag 700  
cagcaactacc ggctgtgcaa tggatgtcc aaccgcttct gggctgggg 750  
ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800  
tttccgccc ctcggaaatc acaactgggt acaagacatt tcgcccacctg 850  
catgaccagg cctggcgaa gagggaccag aagcgcatcg cagctaaaaa 900  
acaggaggcag ttcaagggtgg acagggaggg aggccctgaac actgtgaagt 950  
accatgtggc ttcccgact gcctgtctg tggcggggc cccctgcact 1000  
gtcctcaaca tcatgttggc ctgtgacaag accgccacac cctggtgac 1050  
attcagctga gctggatggc cagtggaa gcctgtacct acaggccata 1100  
ttgctcaggc tcaggacaag gcctcaggc gtggcccgag ctctgacagg 1150  
atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagccaccc 1200  
ggccgccaag gcaggcttgg gctggcccgag gacacgtggg gtgcctggg 1250  
cgctgcttgc catgcacagt gatcagagag aggctgggt gtgtcctgtc 1300  
cgggaccccc cctgccttcc tgctcacctt actctgaccc cttcacgtg 1350  
cccaggcctg tggtagtgg ggagggctga acaggacaac ctctcatcac 1400  
cctactctga ctccttcac gtgccaggc ctgtggtag tggggaggc 1450  
tgaacaggac aacctctcat caccggaaaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
<211> 327  
<212> PRT  
<213> Homo sapiens  
  
<220>

<221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.  
  
 <220>  
 <221> misc\_feature  
 <222> 19-25, 65-71, 247-253, 285-291, 303-310  
 <223> N-myristoylation site.  
  
 <220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.  
  
 <220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).  
  
 <220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.  
  
 <220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.  
  
 <400> 17  

Met	Phe	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln	Leu	Pro	Trp	Glu	Asp
1				5					10				15	

  

Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	Arg	Lys	Cys	Ser
	20					25							30	

  

Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	Phe	Phe	Ser
		35					40						45	

  

Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala
			50				55					60		

  

Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys
	65					70						75		

  

Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp
		80						85					90	

  

Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe
		95						100					105	

  

Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser
			110					115					120	

  

Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp
			125						130				135	

  

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp		
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala		
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His		
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His		
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly		
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu		
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe		
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg		
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly		
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu		
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp		
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser		
320	325	

<210> 18  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 18  
 gcgaacgctt cgaggagtcc tgg 23

<210> 19  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

<222> 1-24  
<223> Synthetic construct

<400> 19  
gcagtgcggg aagccacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 20  
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
caatgttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50  
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100  
gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150  
gattgggcct tctttcccccc ttcccttctg tgtctcctgc ctcatcggcc 200  
tgccatgacc tgcagccaag cccagcccg tgggaaggg gagaaaagtgg 250  
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300  
ggctaggggg gctgccttat ttaaagtggt tgtttatgat tcttatacta 350  
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450  
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22  
<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-15  
<223> Signal peptide.

<220>  
<221> misc\_feature  
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met	Leu	Leu	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Lys	Gly		
1					5				10			15		
Ser	Cys	Leu	Glu	Trp	Gly	Leu	Val	Gly	Ala	Gln	Lys	Val	Ser	Ser
					20				25			30		
Ala	Thr	Asp	Ala	Pro	Ile	Arg	Asp	Trp	Ala	Phe	Phe	Pro	Pro	Ser
					35				40			45		
Phe	Leu	Cys	Leu	Leu	Pro	His	Arg	Pro	Ala	Met	Thr	Cys	Ser	Gln
					50				55			60		
Ala	Gln	Pro	Arg	Gly	Glu	Gly	Glu	Lys	Val	Gly	Asp	Gly		
					65				70					

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

gggacccatg cggccgtgac ccccggtccc ctagaggccc agcgcagccg 50  
cagcggacaa aggagcatgt ccgcgcgggg gaaggccctt cctccggccg 100  
ccataaggct ccggtcgcgg ctgggccccgc gccgcgcctcc tgcccgccccg 150  
ggctccgggg cgccccgcta ggccagtgcg ccgcccgtcg ccccgccaggc 200  
cccgccccgc agcatggagc caccggacg ccggcggggc cgccgcgcagc 250  
cgccgctgtt gctgccgttc tcgcgttttag cgctgctcgc gctgctggga 300  
ggcggccggcg gcggccggcgc cgccgcgtcg cccgcccgt gcaagcacga 350  
tggccggccc cgaggggctg gcagggcggc gggccccc gagggcaagg 400  
tggtgtgcag cagcctggaa ctcgcgcagg tcctgcccc agatactctg 450  
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500  
gaagaatggc tcattttctg ggttaagtct ctttgcggcc 550  
gaaacaatct tatttagtagt atagatccag gtgccttctg gggactgtca 600  
tctctaaaaa gattggatct gacaaacaat cgaatagat gtctgaatgc 650  
agacatattt cgaggactca ccaatctggt tcggctaaac ctttcgggg 700  
atttgttttc ttcatatatct caaggaactt ttgattatct tgcgtcatta 750  
cggtctttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800  
gtggatgcat cgctggtaa aggagaagaa catcacgta cgggatacca 850

ggttgtttt tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900  
caggagctgt tgacatgcga ccctccgctt gaattgccgt ctttctacat 950  
gactccatct catcgccaag ttgtgttga aggagacagc cttccttcc 1000  
agtgcattgc ttcatatatatt gatcaggaca tgcaagtgtt gtggtatcag 1050  
gatgggagaa tagttgaaaac cgatgaatcg caaggtattt ttgttgaaaa 1100  
gaacatgatt cacaactgct ctttgattgc aagtgcctta accatttcta 1150  
atattcaggg tggatctact ggaaattggg gctgtcatgt ccagacccaa 1200  
cgtggaaata atacgaggac tgtggatatt gtggtatttag agagttctgc 1250  
acagtaactgt cctccagaga gggtggtaaa caacaaaggt gacttcagat 1300  
ggcccagaac attggcaggc attactgcat atctgcagtg tacgcggAAC 1350  
acccatggca gtgggatata tcccgaaac ccacaggatg agagaaaAGC 1400  
ttggcgcaga tgtgatagag gtggctttt ggcagatgat gattattctc 1450  
gctgtcagta tgcaaatgat gtcactagag ttctttatat gtttaatcag 1500  
atgcccctca atcttaccaa tgccgtggca acagctcgac agttactggc 1550  
ttacactgtg gaagcagcca acttttctga caaaatggat gttatattt 1600  
tggcagaaat gattgaaaaaa ttggaaagat ttaccaagga ggaaaaatca 1650  
aaagagctag gtgacgtgat gttgacatt gcaagtaaca tcatgttggc 1700  
tcatgttggc gtcctgtggc tggcgcagag ggaagctaaa gcctgcagta 1750  
ggattgtgca gtgtcttcag cgcatggcta cctaccggct agccggtgga 1800  
gctcacgtt attcaacata ttccaccaat attgctctgg aagcttatgt 1850  
catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaag 1900  
tggcagcctc tgatcgtaca ggactttcg attatggag gcgggatcca 1950  
gagggaaacc tggataagca gctgagctt aagtgcata tttcaaatAC 2000  
attttcgagt ctggcactaa aggtatgtt cattctgcaa tcatttaaga 2050  
ctatttacag ttaaatttAga atgctccaaa tggatcgtt cgccaaataa 2100  
ccttattaaa agatTTTttt ttgcaggaag ataggtatta ttgcTTTgc 2150  
tactgttttA aagaaaacta accaggaaga actgcattac gactttcaag 2200  
ggcccttaggc attttgcct ttgattccct ttcttcacat aaaaatatca 2250  
gaaattacat ttataactq caqtqotata aatgcaata tactattgtt 2300

acatgtgaaa aaattttatt tgacttaaaa gtttatttat ttgtttttt 2350  
gctcctgatt ttaagacaat aagatgttt catggccccc taaaagtatc 2400  
atgagcctt ggcactgcgc ctgccaagcc tagtgagaa gtcaaccctg 2450  
agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500  
acacaaatat gtcataatc ttttttaaa aaaagtattt cattgaagca 2550  
agcaaaatga aagcattttt actgattttt aaaattggtg cttagatat 2600  
atttgactac actgtattga agcaaataga ggaggcacaa ctccagcacc 2650  
ctaatttgaac cacattttt tcacttagct ttctgtggc atgtgtatt 2700  
gtattctctg cggttttaa tctcacagta ctttatttct gtcttgtccc 2750  
tcaataatat cacaaacaat attccagtca ttttaatggc tgcataataa 2800  
ctgatccaac aggtgttagg tttctgggt tagtgtgagc actcaataaa 2850  
tattgaatga atgaacgaaa aaaaaaaaaaaa aaa 2883

<210> 24  
<211> 616  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-33  
<223> Signal peptide.

<220>  
<221> TRANSMEM  
<222> 13-40  
<223> Transmembrane domain (type II).

<400> 24  
Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu  
1 5 10 15  
  
Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly  
20 25 30  
  
Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His  
35 40 45  
  
Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
50 55 60  
  
Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
65 70 75  
  
Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
80 85 90

Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser
							95			100				105
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile
							110			115				120
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp
							125			130				135
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg
							140			145				150
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe
							155			160				165
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg
							170			175				180
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile
							185			190				195
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg
							200			205				210
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val
							215			220				225
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu
							230			235				240
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe
							245			250				255
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp
							260			265				270
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu
							275			280				285
Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Glu	Lys	Asn	Met	Ile	His
							290			295				300
Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln
							305			310				315
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg
							320			325				330
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser
							335			340				345
Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp
							350			355				360
Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln
							365			370				375
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro

380	385	390
Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe 395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val 410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr 425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu 440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu 455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys 470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu 485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala 500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg 515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile 530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met 545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly 560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys 575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu 590	595	600
Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr 605	610	615

Ser

<210> 25  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24

<223> Synthetic construct

<400> 25  
gaggactcac caatctggtt cggc 24

<210> 26  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 26  
aactggaaag gaaggctgtc tccc 24

<210> 27  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 27  
gtaaaaggaga agaacatcac ggtacggat accaggtgt tttatcctaa 50

<210> 28  
<211> 683  
<212> DNA  
<213> Homo sapiens

<400> 28  
gcgtggggat gtctaggagc tcgaaggtgg tgctgggcct ctcggtgctg 50  
ctgacggcgg ccacagtggc cggcgtaat gtgaagcagc agtgggacca 100  
gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgg 150  
aaaaagaaaa cattcgtctt ttgggagaac agattatttt gactgagcaa 200  
cttgaagcag aaagagagaa gatgttattt gcaaaaggat ctcaaaaatc 250  
atgacttcaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtgt 300  
gtgtgttcat ggagagtagc ttagtagtat cttcatctt tttttggtc 350  
actgtccctt taaacttcat caaataaagg acagtggtc atataagtta 400  
ctgcttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450  
tttggaaagag tctgtctgg tgatcctggt agaagccccca ttagggtcac 500  
tgtccagtgc ttaggggtgt tactgagaag cactgccgag cttgtgagaa 550

ggaaggatg gatagtagca tccacctgag tagtctgatc agtcggcatg 600  
atgacgaagc cacgagaaca tcgacacctag aaggactgga ggaaggtgaa 650  
gtggagggag agacgctcct gatcgctgaa tcc 683

<210> 29  
<211> 81  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-21  
<223> Signal peptide.

<400> 29  
Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu  
1 5 10 15  
Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp  
20 25 30  
Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln  
35 40 45  
Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
50 55 60  
Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala  
65 70 75  
Lys Gly Ser Gln Lys Ser  
80

<210> 30  
<211> 2128  
<212> DNA  
<213> Homo sapiens

<400> 30  
ctgtcgtctt tgcttcagcc gcagtcgcca ctggctgcct gaggtgctct 50  
tacagcctgt tccaagtgtg gcttaatccg tctccaccac cagatcttc 100  
tccgtggatt cctctgtcaa gaccgctgcc atgccagtga cggttaacccg 150  
caccaccatc acaaccacca cgacgtcatc ttccggcctg gggccccca 200  
tgatcgtggg gtccccctcggtt gcccgtacac agccccctggg tctcccttcgc 250  
ctgctgcagc tggtgtctac ctgcgtggcc ttctcgctgg tggctagcgt 300  
gggcgcctgg acggggtcca tggcaactg gtccatgttc acctggtgct 350  
tctgcttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400  
caggccccgtt tccccctgtc ttggcgcaac ttccccatca ctttcgcctg 450

ctatcgccc ctcttctgcc tctcggcc tc catcat tac cccaccac 500  
atgtccagtt cctgtccc ac ggccggttc gc gggaccac gc catcgccgc 550  
ac cttcttct cctgc atc gc gtgtgtgg ct tac gcc accg aagtggcctg 600  
gacccggcc cggccggcg agatcactgg ctatatggcc accgtacccg 650  
ggctgctgaa ggtgctggag ac cttcg ttg cctgc atc cat cttcg cgttc 700  
atc agc gacc cca ac ctg ta cc agc acc ag ccggccct gg agtgg tgc gt 750  
ggc ggtgtac gcc atc tg ct ac tcc tag c gcc atc gcc atc ctg ctg a 800  
ac ctggggga gtgc acca ac gtgc tacc ca tccc cttccc cagttc ctg 850  
tcggggctgg cttg ctg tc tgc ctc tatgc caccg cccttgtt ct 900  
ctggcccctc tacc agt tcg atgaga agta tggc gggccag cctc gggc gt 950  
cgagagatgt aagctgc agc cg cagccatg cctacta cgt gtgtgc ctgg 1000  
gaccgccc ac tgg ctgt gg c catc ctg acg gcc atc aacc tact gg cgt a 1050  
tgtggctg ac ctgg tgc act ctg ccc ac ct gg tttt gtc aagg tcta ag 1100  
act ctcc caa gagg ctcc cg ttcc ctcc aac ct ct tg tt ct ct tg c 1150  
ccg agt tttc ttat gg agt act tttt cc tcc gc ct ttc ct atg tttc 1200  
ctcttcc tgc tccccc tccca cttt ttctt cc tt ccaatt ct 1250  
tgca ct ct aa cc agt tctt g gatc atc tttt cc tt cc tt tg 1300  
ctgtttcc tt cctgtgtgt tttt gg ccc acat cctg tt tt cacc cctg 1350  
agctgttt ct tttt ct tt tctt tttt tttt tttt tttt aagac g 1400  
gattctca ct gtggccca ggctggagtg cag tgg tgc g atc tca gctc 1450  
actgca accc ccgc ct cc tg gg tca aagc g att ct cc tcc ccc agc ct cc 1500  
caagtagctg ggaggacagg tgtgagctgc cgc accc agc ctgttt ct ct 1550  
ttttccactc ttctttt tc atc tctt tctg ggtt gc ctgtc ggctt 1600  
tcttatctgc ctgtttgca agc ac ct tct cctgtgtc ct tgg agccct 1650  
gagacttctt tctatc ct tg cctt g cttcc ac ccca agg tgctg agctc 1700  
acatccacac cccttgc agc cgtccatg cc ac agcccccc aaggggcccc 1750  
attgcca aag catgc ctg cc cacc ct cgt gtgc ctt tagt cag tgc tgc ac 1800  
gtgtgtgtgt gtgtgtgttt ggggggtggg ggg tgg ggtag ctggggattg 1850  
ggccctt ctccca ggttgg agga aggtgt gtact cccctttaa 1900

attaaaaaac atatatataat atatattgg aggtcagtaa tttccaatgg 1950  
 gcgggaggca ttaagcaccc accctgggtc cctaggcccc gcctggcact 2000  
 cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050  
 ccactgccta gaggccatct taaaggaagc aggggctgga tgccttcat 2100  
 cccaaactatt ctctgtggta tgaaaaag 2128

<210> 31  
 <211> 322  
 <212> PRT  
 <213> Homo sapiens

<400> 31  
 Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr  
 1 5 10 15

Ser	Ser	Ser	Gly	Leu	Gly	Ser	Pro	Met	Ile	Val	Gly	Ser	Pro	Arg
				20					25					30

Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val
				35				40						45

Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp
			50					55						60

Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys
			65					70						75

Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu
				80				85						90

Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe
				95				100						105

Ala	Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr
				110				115						120

Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp
				125				130						135

His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala
				140				145						150

Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile
				155				160						165

Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu
				170				175						180

Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn
				185				190						195

Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu	Glu	Trp	Cys	Val	Ala	Val	Tyr
				200				205						210

Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu
				215					220					225
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu
				230					235					240
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu
				245				250						255
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln
				260				265						270
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr
				275				280						285
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr
				290				295						300
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala
				305				310						315
His	Leu	Val	Phe	Val	Lys	Val								
				320										

<210> 32  
 <211> 3680  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
 gaacgtgcca ccatgcccaag ctaatttttgc tatttttagt agagacgggg 50  
 ttccaccatg ttggccaggc tggcttgaa ctcgtgacct catgatccgc 100  
 tcaccccgcc ctccccaaagt gctgggatta caggcatgag ccactgacgc 150  
 ctggccagcc tatgcatttt taagaaatta ttctgttata ggtgctgtgc 200  
 taaacattgg gcactacagt gaccaaaaaca gactgaattc cccaaagagcc 250  
 aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300  
 ttattactca ctatgactaa gggtcacaaa tggggtaactg tgatggagag 350  
 tgatttgtta agagactaca gagggaggac agactaccaa gaggggggccc 400  
 aggaaagctc ctctgacgag gtggatttc agcccaaact ggaagaatga 450  
 gaaagagcta gccagccatc agaatagtcc agaagagatg gggagcacta 500  
 cactcactac actttggcct gagaaaaatag catgggattg gaggaggctg 550  
 ggggaacacc acttctgccc acctggcag gaggcattga gggcttgaga 600  
 aaggcataatg gcagtagcag tagaaaggac aggtaggag cagggacttt 650  
 gcaggtggaa tcatttagtc ttatcaacag atatggcaa gcaaagccag 700

gggagaattg atggtaatgc tgaggtttg agccaggcta gatgggacag 750  
tggtgtgtga tgcaaaggaa agaggtcagg aagcagggcc agacgtgggg 800  
agaaggtgtg ggggttttgtt ttccatcttg ccgagtctgc cggaatgtgg 850  
atggaaagac caagaggagg agcaaggggc agaggggaag ggaatcttaa 900  
agaagtccctg gatgccacac tcttcttcct tcctcctctt ccctctcc 950  
agaggtctca ctcgtggttc ttcatttcct gccctgcctc catctcctct 1000  
gggtgctggg aaagtggagg attagctgaa gtttgcttc tcggggcctg 1050  
tctgaatctc cattgcttcc tggaggaca taattcacct gtcctagctt 1100  
cttatcatct tacatttccc tgtagccact gggacatatg tgggtttcct 1150  
tcctagctcc tgtctcctcc tcatgcctt gctgggtatg ggcatgttag 1200  
gggaaaggc attgctgtca gaggggcact gactttctaa tgggtttacc 1250  
caaggtaat gttggagaca cagtcgcgt gctgccaag tcccgccgag 1300  
ccctaactat ccaggagatc gctgcgcgtt ccaggtccctc cctgcattgtt 1350  
atgcagcccc tcccatgttt ctggccactt tgtccttct cctccgttt 1400  
gcacatccct ttggaactgt ttccatgtgag tacatgctgg ggtctccct 1450  
ttctccctt gtcaggtga atctcagccc cttctccac ccaaagggttc 1500  
acatggatcc taactactgc cacccttcca cctccctgca cctgtgctcc 1550  
ctggcctggt cctttaccag gcttctccac cctccctat ctccaggtat 1600  
ttcccaggtg gtgaaggacc acgtgaccaa gcctaccgcc atggcccagg 1650  
gccgagtggc tcacctcatt gagtggagg gctggagcaa gccgagtgac 1700  
tcacctgctg ccctggaatc agcctttcc tcctattcag acctcagcga 1750  
gggcgaacaa gaggctcgct ttgcagcagg agtggctgag cagtttgcca 1800  
tcgcggaagc caagctccga gcatggtctt cgggtggatgg cgaggactcc 1850  
actgatgact cctatgatga ggactttgct ggggaatgg acacagacat 1900  
ggctggcag ctgccccctgg ggccgcacct ccaggacctg ttccacccggcc 1950  
accggttctc cggccctgtg cggcagggtc ccgtggagcc tgagagcgcac 2000  
tgctcacaga ccgtgtcccc agacaccctg tgctctagtc tgtgcagcct 2050  
ggaggatggg ttgttgggct ccccgccccg gctggcctcc cagctgctgg 2100  
gcgatgagct gcttctcgcc aaactgcccc ccagccggga aagtgccttc 2150

cgcagcctgg gcccaactgga ggcccaggac tcactctaca actcgccct 2200  
cacagagtcc tgcctttccc ccgcggagga ggagccagcc ccctgcaagg 2250  
actgccagcc actctgccc ccactaacgg gcagctggga acggcagcgg 2300  
caagcctctg acctggcctc ttctgggtg gtgtccttag atgaggatga 2350  
ggcagagcca gaggaacagt gaccacatc atgcctggca gtggcatgca 2400  
tccccggct gctgccaggg gcagagcctc tgtgccaag tgtggctca 2450  
aggctcccag cagagctcca cagcctagag ggctcctggg agcgctcgct 2500  
tctccgttgt gtgtttgca taaaatgtttt tggagaggag gcaggggctg 2550  
ggctgggggc gcatgtcctg ccccaactcc cggggcttgc cgggggttgc 2600  
ccggggcctc tggggcatgg ctacagctgt ggcagacagt gatgttcatt 2650  
ttcttaaaat gccacacaca catttcctcc tcggataatg tgaaccacta 2700  
agggggttgt gactgggctg tgtgagggtg ggggtggagg gggcccagca 2750  
accccccacc ctcggccatgc ctctcttttc tctgcttttc ttctcacttc 2800  
cgagtccatg tgcaatgcgtt gatagaatca ccccccacctg gaggggctgg 2850  
ctcctgccc cccggagcct atgggttgag ccgtccctca agggcccctg 2900  
cccaagctggg ctcgtgctgt gcttcattca cctctccatc gtctctaaat 2950  
cttcctcttt ttccctaaatg acagaagggtt tttgggtctgt ttttcagtc 3000  
ggatcttctc ttctctggga ggctttggaa tggatgaaagc atgtaccctc 3050  
cacccttttc ctggcccccct aatggggcct gggcccttcc ccaaccctc 3100  
ctaggatgtg cgggcagtgt gctggcgcct cacagccagc cgggctgccc 3150  
attcacgcag agctctctga gcgggaggtg gaagaaagga tggctctgg 3200  
tgccacagag ctgggacttc atgttcttct agagagggcc acaagagggc 3250  
cacaggggtg gccgggagtt gtcagctgat gcctgctgag aggcaaggt 3300  
tgtgccagtg agtgcacatc atgagggtgt gtctcttctt ggggaggaaa 3350  
gaaggttagag cctttctgtc tgaatgaaag gccaaggcta cagtaggg 3400  
ccccggccca gccagggtgt taatgcccac gtagtggagg cctctggcag 3450  
atcctgcatt ccaagggtcac tggactgtac gtttttatgg ttgtggaaag 3500  
ggtgggtggc tttagaatta agggccttgc aggcttggc aggtaaagg 3550  
gcccaaggta agaacgagag ccaacgggca caagcattct atatataagt 3600

ggctcattag gtgtttatTT tgTTCTATT aagaatttGT tttattaaAT 3650  
 taatataaaaa atctttgtAA atctctaaaa 3680

<210> 33  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<400> 33  
 Met Phe Leu Ala Thr Leu Ser Phe Leu Leu Pro Phe Ala His Pro  
   1               5               10               15

Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser  
   20              25              30

Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val  
   35              40              45

His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu  
   50              55              60

Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu  
   65              70              75

Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro  
   80              85              90

Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys  
   95              100             105

Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala  
   110             115             120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg  
   125             130             135

Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys  
   140             145             150

Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp  
   155             160             165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala  
   170             175             180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly  
   185             190             195

His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu  
   200             205             210

Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser  
   215             220             225

Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu  
   230             235             240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro  
245 250 255  
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala  
260 265 270  
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser  
275 280 285  
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu  
290 295 300  
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser  
305 310 315  
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala  
320 325 330  
Glu Pro Glu Glu Gln  
335

<210> 34  
<211> 25  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct  
  
<400> 34  
tgtccttgc cccagacttc tgtcc 25  
  
<210> 35  
<211> 50  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.  
  
<400> 35  
ctggatgcta atgtgtccag taaatgatcc ccttatcccc tcgcgatgct 50  
  
<210> 36  
<211> 25  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.  
  
<400> 36

ttccactcaa tgaggtgagc cactc 25  
<210> 37  
<211> 23  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-23  
<223> Synthetic construct.  
  
<400> 37  
ggcgagccct aactatccag gag 23  
  
<210> 38  
<211> 39  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-39  
<223> Synthetic construct.  
  
<400> 38  
ggagatcgct gcgctggcca ggtcctccct gcatggtat 39  
  
<210> 39  
<211> 22  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.  
  
<400> 39  
ctgctgcaaa gcgagcctct tg 22  
  
<210> 40  
<211> 2084  
<212> DNA  
<213> Homo sapiens  
  
<400> 40  
ggtcctggg cgctctgtta cacaagcaag atacagccag ccccacctaa 50  
tttgcgtttcc ctggcacccct cctgctcaagt gcgacattgt cacacttaac 100  
ccatctgttt tctctaattgc acgacagatt ccttcagac aggacaactg 150  
tgatatttca gttcctgatt gtaaataacct cctaagcctg aagcttctgt 200  
tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250  
caatctattc ttgccacatc aaggattgt tattccttta aaaaaaaaaacc 300

aataccaaag aagcctacaa tggtggcatt agccaaaatt ctgttgattt 350  
caacgttggtt ttattcactt ctatcgaaaa gccatggaaa agaaaatcaa 400  
gacataaaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450  
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500  
atataaccac ctcaaatctc aaggcgagtc attcccctcc tttgaatcta 550  
cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600  
gcattcttg ggcagtctaa aacccacatc taccattcc acaagccctc 650  
ccttgatcca tagcttggtt tctaaagtgc cttggaatgc acctatagca 700  
gatgaagatc ttttgcccat ctcagcacat cccaatgcta cacctgctct 750  
gtcttcagaa aacttcactt ggtcttggtt caatgacacc gtgaaaactc 800  
ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850  
ccatctgtga ccccccttgat agtggAACCA agtggatggc ttaccacaaa 900  
cagtgatagc ttcaactgggt ttaccctta tcaagaaaaa acaactctac 950  
agcctacctt aaaattcacc aataattcaa aactcttcc aaatacgtca 1000  
gatccccaaa aagaaaaatag aaatacagga atagtattcg gggccatttt 1050  
aggtgctatt ctgggtgtct cattgcttac tcttgtggc tacttgggtt 1100  
gtggaaaaag gaaaacggat tcattttccc atcggcgact ttatgacgac 1150  
agaaatgaac cagttctgct attagacaat gcaccggAACCTT cttatgatgt 1200  
gagttttggg aattcttagct actacaatcc aactttgaat gattcagcca 1250  
tgccagaaaag tgaagaaaaat gcacgtgatg gcattcctat ggatgacata 1300  
cctccacttc gtacttctgt atagaactaa cagaaaaag gcgttaaaca 1350  
gcaagtgtca tctacatcct agcctttga caaattcatc tttcaaaagg 1400  
ttacacaaaa ttactgtcac gtggattttg tcaaggagaa tcataaaagc 1450  
aggagaccag tagcagaaaat gtagacagga tgtatcatcc aaaggTTTC 1500  
tttcttacaa ttttggcca tcctgaggca tttactaagt agccttaatt 1550  
tgtatTTAG tagtattttc ttagtagaaa atatttggtt aatcagataa 1600  
aactaaaaaga ttccaccatt acagccctgc ctcataacta aataataaaa 1650  
attattccac caaaaaattc taaaacaatg aagatgactc tttactgctc 1700  
tgcctgaagc cctagtagcca taattcaaga ttgcatttc ttaaatgaaa 1750

attgaaaggg tgcttttaa agaaaatttgc acttaaagct aaaaagagga 1800  
catagccca agtttctgtt attggaaat tgaggcaata gaaatgacag 1850  
acctgtattc tagtacgtta taatttctca gatcagcaca cacatgatca 1900  
gcccaactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950  
aggaaagctg accctaccca ggaaaagtaat agcttcttta aaagtcttca 2000  
aagggtttgg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050  
ttgggtgcct taaaaactca atgagaatca tgg 2084

<210> 41  
<211> 334  
<212> PRT  
<213> *Homo sapiens*

<400> 41  
 Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr  
 1 5 10 15  
  
 Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn  
 20 25 30  
  
 Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
 35 40 45  
  
 Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
 50 55 60  
  
 Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
 65 70 75  
  
 Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
 80 85 90  
  
 Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
 95 100 105  
  
 Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val  
 110 115 120  
  
 Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser  
 125 130 135  
  
 Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr  
 140 145 150  
  
 Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser  
 155 160 165  
  
 Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val  
 170 175 180  
  
 Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser  
 185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu  
200 205 210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn  
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe  
230 235 240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu  
245 250 255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser  
260 265 270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu  
275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser  
290 295 300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu  
305 310 315

Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu  
320 325 330

Arg Thr Ser Val

<210> 42  
<211> 1594  
<212> DNA  
<213> Homo sapiens

<400> 42  
aacaggatct cctcttgcag tctgcagccc aggacgctga ttccagcagc 50  
gccttaccgc gcagccccaa gattcaatat ggtgaaaatc gccttcaata 100  
ccccctaccgc cgtgcaaaaag gaggaggcgc ggcaagacgt ggaggccctc 150  
ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200  
tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttaactct 250  
taggccttcc attcatcttgcaggactta ttgttggtgg agcctgcatt 300  
tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350  
ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400  
tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450  
atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500  
tattcatgac tttgaaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgccctcaataactt ctattgttat gcctccaaaa 600  
aatctggtag agctcttgg caaactggcg agtggcagat atctgcctca 650  
aacttatgtg gttcgagaag acctagttgc tgtggaggaa attcgtgatg 700  
ttagtaacct tggcatctt atttaccaac tttgcaataa cagaaagtcc 750  
ttccgccttc gtgcagaga cctcttgctg ggtttcaaca aacgtgccat 800  
tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850  
ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900  
agaagtcaga gatttacaat atgactttaa cattaagggtt tatgggatac 950  
tcaagatatt tactcatgca tttactctat tgcttatgct taaaaaaaaag 1000  
aaaaaaaaaaa aaaactacta accactgcaa gctcttgta aatttttagtt 1050  
taattggcat tgcttgcccc ttgaaaactga aattacatga gtttcatttt 1100  
ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150  
cctaacatcc tgacaataaa ttccatccgt tgttttttt gtttgttgt 1200  
tttttctttt ccttaagta agctcttcat tcattttatg gtggagcaat 1250  
tttaaaattt gaaatatttt aaattgtttt tgaactttt gtgtaaaata 1300  
tatcagatct caacattgtt ggtttctttt gtttttcatt ttgtacaact 1350  
ttcttgaatt tagaaattac atcttgcag ttctgttagg tgctctgtaa 1400  
ttaacctgac ttatatgtga acaatttca tgagacagtc atttttaact 1450  
aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500  
tgtgttaggtg ctgaatgctg taaggagttt aggttgtatg aattctacaa 1550  
ccctataata aattttactc tataaaaaaa aaaaaaaaaa aaaa 1594

<210> 43  
<211> 263  
<212> PRT  
<213> Homo sapiens

<400> 43  
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu  
1 5 10 15  
Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg  
20 25 30  
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu  
35 40 45  
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly	Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys		
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu		
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp		
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp		
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr		
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu		
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe		
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val		
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn		
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe		
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala		
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile		
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 44  
gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 45  
gggaaactgct atctgatgcc 20

<210> 46  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 46  
caggatctcc tcttgcagtc tgcagc 26

<210> 47  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 47  
cttctcgAAC cacataagtt tgaggcag 28

<210> 48  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 48  
cacgattccc tccacagcaa ctggg 25

<210> 49  
<211> 1969  
<212> DNA  
<213> Homo sapiens

<400> 49  
ggaggaggga gggcgggcag gcGCCAGCCC agAGCAGCCC cgggcaccag 50

cacggactct ctcttccagc ccaggtgccc cccactctcg ctccattcgg 100  
cgggagcacc cagtccctgta cgccaaggaa ctggtcctgg gggcaccatg 150  
gtttcggcgg cagccccag cctcctcatc cttctgttgc tgctgctggg 200  
gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250  
tggaggatgt ggcgggtagt ggggaggccg agggctcgtc gcctcctcc 300  
ccgagcctcc cgccaccctg gacccggcc ctcagccca catcgatggg 350  
gcccccagccc acaaccctgg gggcccatc accccccacc aacttcctgg 400  
atgggatagt ggacttcttc cgccagtacg tcatgtat tgctgtggg 450  
ggctccctgg ctttctgct gatgttcatc gtctgtgccg cggtcatcac 500  
ccggcagaag cagaaggcct cgccctatta cccatcgcc ttccccaaaga 550  
agaagtacgt ggaccagagt gaccggccg ggggcccccg ggccttcaagt 600  
gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650  
ctcccgccag ctccaggccg acatcttggc cgccaccctg aacctcaagt 700  
cccccaccag ggctgcactg ggccgtgggg acggagccag gatggtgag 750  
ggcagggcgc cagaggaaga ggagaaggc agccaggagg gggaccagga 800  
agtccaggga catgggttcc cagtggagac accagaggcg caggaggagc 850  
cgtgctcagg ggtcctttag gggctgtgg tggccggta gggcaagg 900  
gagctggaag ggtctcttt gttagccag gaagcccagg gaccagtggg 950  
tccccccgaa agccctgtg cttgcagcag tgtccacccc agtgtctaac 1000  
agtccctcccg ggctgccagc cctgactgtc gggccccc aa gtggtcaccc 1050  
ccccgtgtat gaaaaggcct tcagccctga ctgcttcctg acactccctc 1100  
cttggcctcc ctgtgggtgcc aatcccagca tgtgctgatt ctacagcagg 1150  
cagaaatgct ggtccccgtt gccccggagg aatcttacca agtgcacca 1200  
tccttcaccc cagcagcccc aaagggtac atcctacagc acagctcccc 1250  
tgacaaagtg agggaggcga cgtgtccctg tgacagccag gataaaacat 1300  
cccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaacc 1350  
tacttttaa aacagctaca ggtaaaatc ctgcagcacc cactctggaa 1400  
aatactgctc ttaattttcc tgaagggtggc cccctgttcc tagttggtcc 1450  
aggatttaggg atgtgggta tagggcattt aaatcctctc aagcgctctc 1500

caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550  
gatcagggttg aatgaatgga acttttcctg tctggcctcc aaagcagcct 1600  
agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650  
ggggctgggg aagggtttct gacgcccagc ctggagcagg gggccctgg 1700  
ccacccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750  
gtcagtcctc gacagggagc ctgggctccg tcctgcttta gggaggctct 1800  
ggcaggaggt cctctccccat ccctccat ctggggctcc cccaacctct 1850  
gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900  
attccggcct gaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaa 1950  
aaaaaaaaaaa aaaaaaaaga 1969

<210> 50  
<211> 283  
<212> PRT  
<213> Homo sapiens

<400> 50  
Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu  
1 5 10 15  
Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu  
20 25 30  
Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
35 40 45  
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
50 55 60  
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
65 70 75  
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe  
80 85 90  
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala  
95 100 105  
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln  
110 115 120  
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys  
125 130 135  
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe  
140 145 150  
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala  
155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr
														180
170														
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
														195
185														
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
														210
200														
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
														225
215														
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
														240
230														
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
														255
245														
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
														270
260														
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val		
275														
280														

<210> 51  
<211> 1734  
<212> DNA  
<213> Homo sapiens

<400> 51  
gtggactctg agaagccca gtcaggatggg acaggagaga gaaggctgca 50  
gaccaggagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100  
gcacagagac gcagagcaag ggcggcaagg aggagacctt ggtggagga 150  
agacactctg gagagagagg gggctggca gagatgaagt tccaggggcc 200  
cctggcctgc ctcctgctgg ccctctgcct gggcagtgccc gaggctggcc 250  
ccctgcagag cggagaggaa agcactggaa caaatattgg ggaggccctt 300  
ggacatggcc tgggagacgc cttgagcgaa ggggtggaa aggcattgg 350  
caaagaggcc ggagggggcag ctggctctaa agtcagtgag gcccttggcc 400  
aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggctt 450  
ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500  
gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550  
acggagcaga tgctgtccgc ggctcctggc agggggtgcc tggccacagt 600  
ggtgcttggg aaacttctgg agggcatggc atctttggct ctcaaggtgg 650  
ccttggaggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata cccccgaaac tcagcaggca gctttggaaat gaatcctcag 750  
ggagctccct ggggtcaagg aggcaatggc gggccaccaa actttggac 800  
caacactcag ggagctgtgg cccagcctgg ctatggttca gtgagagcca 850  
gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900  
ggctccagca actctggggg aggcaagcgc tcacagtgg gcagcagtgg 950  
cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000  
gcagtggcag cagcagtggc agcagcagtgc gcggcagcag tggcggcagc 1050  
agtggtggca gcagtggcaa cagtggtggc agcagaggta acagcggcag 1100  
tgagtccctcc tggggatcca gcaccggctc ctcctccggc aaccacggta 1150  
ggagcggcgg aggaaatggc cataaaccgg ggtgtaaaaa gccaggaaat 1200  
gaagcccgcg ggagcggggg atctggatt cagggcttca gaggacaggg 1250  
agtttccagc aacatgaggg aaataagcaa agagggcaat cgcctccttg 1300  
gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgg 1350  
ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400  
tgggatgttt aactttgaca ct当地tggaa gaattttaaa tccaaagctgg 1450  
gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500  
ccgtgacctc cagacaagga gccaccagat tggatggag ccccccacact 1550  
ccctccctaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600  
aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52  
<211> 440  
<212> PRT  
<213> Homo sapiens

<400> 52  
Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys  
1 5 10 15  
Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser  
20 25 30  
Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp  
35 40 45  
Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50	55	60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr		
65	70	75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly		
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala		
95	100	105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val		
110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val		
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile		
140	145	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro		
155	160	165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser		
170	175	180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln		
185	190	195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly		
200	205	210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln		
215	220	225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly		
230	235	240
Ser Ser Asn Ser Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser		
245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly		
260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser		
275	280	285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser		
290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly		
305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His		
320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly		
335	340	345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn  
350 355 360

Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser  
365 370 375

Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly  
380 385 390

Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser  
395 400 405

Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser  
410 415 420

Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg  
425 430 435

Ser Ser Arg Ile Pro  
440

<210> 53

<211> 3580

<212> DNA

<213> Homo sapiens

<400> 53

gaccggccc tccggtcctg gatgtgcgga ctctgctgca gcgaggcgtg 50  
cagggccgcc gggcggtgct caccgtgccc tggctggtgg agtttctctc 100  
ctttgctgac catgttggttc ctttgctgga atattaccgg gacatcttca 150  
ctctcctgct gcgcctgcac cggagcttgg tggctgcga ggagagttag 200  
ggaaagatgt gtttcctgaa caagctgctg ctacttgctg tcctggcgtg 250  
gctttccag attcccacag tccctgagga cttgttcttt ctgaaagagg 300  
gtccctcata tgccttgag gtggacacag tagccccaga gcatggcttg 350  
gacaatgcgc ctgtggtgga ccagcagctg ctctacacct gctgccccta 400  
catcgagag ctccggaaac tgctcgcttc gtgggtgtca ggcagtagtg 450  
gacggagtgg gggcttcatg aggaaaatca ccccccacac taccaccaggc 500  
ctgggagccc agcctccca gaccagccag gggctgcagg cacagctcgc 550  
ccagggcttt ttccacaacc agccggccctc cttgcgcgg accgttagtg 600  
tcgtggcaga aagaattgga tcaaactgtg tcaaacatat caaggctaca 650  
ctgggtggcag atctggtgcg ccaggcagag tcacttctcc aagagcagct 700  
ggtgacacag ggagaggaag ggggagaccc agcccagctg ttggagatct 750  
tgtgttccca gctgtccct cacggggccc aggcattggc cctggggcgg 800

Y  
E  
A  
R  
2  
0  
0  
9  
B  
I  
O  
L  
O  
G  
Y

gagttctgtc aaaggaagag ccctgggct gtgcggcgc tgcttccaga 850  
ggagaccccg gcagccgttc tgagcagtgc agagaacatt gctgtgggc 900  
ttgcaacaga gaaagcctgt gcttggctgt cagccaacat cacagcactg 950  
atcaggaggg aggtgaaagc agcagtgagt cgcacacttc gagcccaggg 1000  
tcctgaacct gctgccccggg gggagcggag gggctgctcc cgccctgac 1050  
tgctctcct tggccgtggg gccacgggac cctgacgagg gagtctccc 1100  
agagcatctg gaacagctcc taggccagct gggccagacg ctgcggtgcc 1150  
gccagttcct gtgcccacct gctgagcagc atctggcaaa gtgctctgtg 1200  
gagttagctt ccctcctcgt tgcaagatcaa attcctatcc tagggccccc 1250  
ggcacagtac aggctggaga gagggcaggc tcgaaggctt ctgcacatgc 1300  
tgcttcctt gtggaaggaa gacttcagg ggccggttcc gctgcagctg 1350  
ctgctgagcc caagaaatgt ggggcttctg gcagacacaa ggccaaggga 1400  
gtgggacttg ctgctattct tgctacggg a gctggtggag aagggtctga 1450  
tgggacggat ggagatagag gcctgcctgg gcagcctcca ccaggccca 1500  
tggccagggg actttgctga agaattagca acactgtcta atctgtttct 1550  
agccgagccc cacctgccag aaccccagct aagaggctgt gagttggtgc 1600  
agccaaaccg gggcactgtg ctggccca gctaggcgtg agaagtggcc 1650  
ctgccttggg cattgcacca gaaccctgga ccccccgcctc acgaggaggg 1700  
ccaagtgccc aatgcagacc ctcactggtt ggggtgttagc tgggtctaca 1750  
gtcagacttc ctgctctaag ggtgtcactg cctggcatcc caccacgcga 1800  
atccttagagg aaggagagtt ggcctgattt gggattatgg cagaaaagtc 1850  
cagagatgcc agtcctggag tagaagaggt ggtgtttgtt tatctcttgg 1900  
atactaaatg aaatgaggtg tgtggcttg tcaacacaga attcaagcct 1950  
catttgctat occagcatct cttaaaaactt tgtagtcttg gaattcatga 2000  
cagaggcaaa tgactcctgc ttaacttatg aagaaagtt aaacatgaat 2050  
cttgggagtc tacattttct tattcaccagg agctggactg ccatttcctt 2100  
ataaaatgcct aacacaggcc gggctgggtg gctcatgcct gtaatcccag 2150  
cactttgaga ggcctgaggt cggcggactg cctgaggtca ggaattcaag 2200  
accagcctgg ccaacatggc aaaaccccat ctctactaaa aataaaaaaa 2250

ttattagctg ggcattggc tgggtgcctg taatcccac tactcaggag 2300  
gatgaggcag gagacactgct tgaacctgga ggtggagggt gcagttagcc 2350  
gaggtcgac cactgcactc cagtcgggt aacagagcga gactttctag 2400  
aaaaaagccta acaaacagat aaggtaggac tcaaccaact gaaacctgac 2450  
tttccccctg taccttcagc ccctgtgcag gtagtaacct cttgagacct 2500  
ctccctgacc agggaccaag cacagggcat ttagagctt tttagaataaa 2550  
ctggttttct ttaaaaaaaaaaaa aaaaaaaaaaaa agggcggccg cccttttttt 2600  
tttttttttt tttttttttt tttttttttt tttttttttt taaaaaggc 2650  
tttttattaaa attctccccca cacatggct cctgcaatct gccacagctc 2700  
tggggcgtgt cctgttaggaa aaggccctgt tttccctgag gcggggctgg 2750  
gcttgcgtccat gggccgcgg agctggccgt gcttggccct ctggcgtgtg 2800  
tctagctgct tcttgcggg cacagagctg cggggctgtt gggcacccggg 2850  
agctaagagc aggctctggt gcaggggtgg aggccctgtct cttaaccgac 2900  
accctgaggt gctcctgaga tgctgggtcc accctgagtg gcacggggag 2950  
cagctgtggc cggtgctcct tcyytaggcca gtcctgggaa aactaagctc 3000  
gggcccctct ttgcaaagac cgaggatggg gtgggtgtgg gggactcatg 3050  
gggaatggcc tgaggagcta cgtgtgaaga gggcgccggt ttgttggctg 3100  
cagcggcctg gagcgcctct ctctgagcc tcagttccc tttccgtcta 3150  
atgaagaaca tgccgtctcg gtgtctcagg gctattagga ctgcgcctca 3200  
ggaagtggcc ttggacgagc gtcatgttat ttccacaact gtcctgcac 3250  
gttggcctgg gcacgtcatg gaatggccca tgtccctctg ctgcgtggac 3300  
gtcgcggcgtcg ggagtgcgcgca gcccaggccg gggccagacg tgcgcctggg 3350  
ggtgaggggaa ggcgcggccgg gagggcctca caggaagttt ggctcccgca 3400  
ccaccaggca gggcgccgtc ccgcgcgcgc cgcgcaccc accgtccagg 3450  
ggccggtaga caaatggaa gtcgcgttg ggctcgctgc gcagcaggta 3500  
gcccttgatg cagtgcggca ggcgcgtc cgcgcgtgg aagcagcgcc 3550  
cgtccaccag cacgaacagc cggcgcgtc 3580

<210> 54  
<211> 280  
<212> PRT  
<213> Homo sapiens

<400> 54

Met	Cys	Phe	Leu	Asn	Lys	Leu	Leu	Leu	Ala	Val	Leu	Gly	Trp
1								10					15
Leu Phe Gln Ile Pro Thr Val Pro Glu Asp Leu Phe Phe Leu Glu													
20 25 30													
Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu													
35 40 45													
His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr													
50 55 60													
Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser													
65 70 75													
Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys													
80 85 90													
Ile Thr Pro Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln													
95 100 105													
Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His													
110 115 120													
Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu													
125 130 135													
Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val													
140 145 150													
Ala Asp Leu Val Arg Gln Ala Glu Ser Leu Leu Gln Glu Gln Leu													
155 160 165													
Val Thr Gln Gly Glu Glu Gly Gly Asp Pro Ala Gln Leu Leu Glu													
170 175 180													
Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala													
185 190 195													
Leu Gly Arg Glu Phe Cys Gln Arg Lys Ser Pro Gly Ala Val Arg													
200 205 210													
Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala													
215 220 225													
Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp													
230 235 240													
Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala													
245 250 255													
Ala Val Ser Arg Thr Leu Arg Ala Gln Gly Pro Glu Pro Ala Ala													
260 265 270													
Arg Gly Glu Arg Arg Gly Cys Ser Arg Ala													
275 280													

<210> 55  
<211> 2401  
<212> DNA  
<213> Homo sapiens

<400> 55  
tccctgaca ggtctggtgg ctggttcggg gtctactgaa ggctgtctt 50  
atcagggaaac tgaagactct ctgctttgc cacagcagtt cctgcagctt 100  
ccttgagggtg tgaacccaca tccctgcccc cagggccacc tgcaggacgc 150  
cgacacacctac ccctcagcag acgccggaga gaaatgagta gcaacaaaga 200  
gcagcggtca gcagtgttcg tgatcctt tgcctcatc accatcctca 250  
tcctctacag ctccaacagt gccaatgagg tcttccatta cggctccctg 300  
cggggccgta gccgccgacc tgtcaacctc aagaagtgga gcatcactga 350  
cggttatgtc cccattctcg gcaacaagac actgccctct cggtgccacc 400  
agtgtgtgat tgtcagcagc tccagccacc tgctggcac caagctggc 450  
cctgagatcg agcgggctga gtgtacaatc cgcatgaatg atgcacccac 500  
caactggctac tcagctgatg tggcaacaa gaccacctac cgcgtcgtgg 550  
cccattccag tgtgttccgc gtgctgagga ggccccagga gtttgtcaac 600  
cggaacctctg aaaccgtgtt catttctgg gggcccccga gcaagatgca 650  
gaagccccag ggcagcctcg tgctgtgat ccagcgagcg ggctgggt 700  
tccccaaacat ggaagcatat gccgtctctc ccggccgcat gcggcaattt 750  
gacgacctct tccggggta gacggcaag gacagggaga agtctcattc 800  
gtggttgagc acaggcttgtt ttaccatggt gatcgccgtg gagttgtgtg 850  
accacgtgca tgtctatggc atggcccccc ccaactactg cagccagcgg 900  
ccccgcctcc agcgcatgcc ctaccactac tacgagccca agggccgg 950  
cgaatgtgtc acctacatcc agaatgagca cagtcgcaag ggcaaccacc 1000  
accgcttcat caccgagaaa agggcttct catcgccggc ccagctgtat 1050  
ggcatcacct tctcccaccc ctccctggacc taggccaccc agcctgtggg 1100  
acctcaggag ggtcagagga gaagcagcct ccggccagcc gctaggccag 1150  
ggaccatctt ctggccaatc aaggcttgct ggagtgtctc ccagccaatc 1200  
agggccttga ggaggatgta tcctccagcc aatcagggcc tggggaatct 1250  
gttggcgaat cagggatttg ggagtctatg tggtaatca ggggtgtctt 1300

tcttgtcag tcagggtctg cgcacagtca atcagggttag agggggattt 1350  
tctgagtcaa tctgaggcta aggacatgtc cttccatg aggcttggt 1400  
tcagagcccc aggaatggac ccccaatca ctccccactc tgctggata 1450  
atgggtcct gtcccaagga gctggaaact tggtgttgc ccctcaattt 1500  
ccagcaccag aaagagagat tgtgtgggg tagaagctgt ctggaggccc 1550  
ggccagagaa tttgtgggt tggaggtt gtggggcggtt tggggaggtc 1600  
ccagaggtgg gaggctggca tccaggtctt ggctctgccc tgagaccttg 1650  
gacaaccct tccccctctc tggcacccct tctgccaca ccagtttcca 1700  
gtgcggagtc tgagaccctt tccacctccc ctacaagtgc cctcgggtct 1750  
gtcctcccg tctggaccct cccagccact atcccttgct ggaaggctca 1800  
gctctttggg gggctctgggg tgacctcccc acctcctgga aaactttagg 1850  
gtatTTTgc gcaaactcct tcagggttgg gggactctga agggaaacggg 1900  
acaaaacctt aagctgttt cttagccct cagccagctg ccattagctt 1950  
ggctcttaaa gggccaggcc tcctttctg ccctctagca gggaggtttt 2000  
ccaactgttg gaggcgcctt tgggctgccc ccttgcgtg gagtcactgg 2050  
gggcttccga gggctccct cgaccctctg tcgtcctggg atggctgtcg 2100  
ggagctgtat cacctgggtt ctgtccctg gctctgtatc aggacttta 2150  
ttaaagctgg gcctcagtgg ggtgttttg tctcctgctc ttctggagcc 2200  
tggaggaaa gggcttcagg aggaggctgt gaggctggag ggaccagatg 2250  
gaggaggcca gcagctagcc attgcacact ggggtgatgg gtggggcggtt 2300  
tgactgcccc agacttggtt ttgtaatgt ttgtacagga ataaacacac 2350  
ctacgctccg gaaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2400  
a 2401

<210> 56  
<211> 299  
<212> PRT  
<213> Homo sapiens

<400> 56  
Met Ser Ser Asn Lys Glu Gln Arg Ser Ala Val Phe Val Ile Leu  
1 5 10 15  
Phe Ala Leu Ile Thr Ile Leu Ile Leu Tyr Ser Ser Asn Ser Ala  
20 25 30

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg
									35					45
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro
									50					60
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val
									65					75
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro
									80					90
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro
									95					105
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg
									110					120
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln
									125					135
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly
									140					150
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val
									155					165
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala
									170					180
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly
									185					195
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr
									200					210
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val
									215					225
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro
									230					240
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro
									245					255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly
									260					270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp
									275					285
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr	
									290					295

<210> 57

<211> 4277

<212> DNA

<213> Homo sapiens

<400> 57

gtttctcata gttggcgtct tctaaaggaa aaacactaaa atgaggaact 50  
cagcgaccg ggagcgacgc agcttgaggg aagcatccct agctgttggc 100  
gcagaggggc gaggctgaag ccgagtggcc cgaggtgtct gaggggctgg 150  
ggcaaaggtg aaagagttc agaacaagct tcctggaacc catgacccat 200  
gaagtcttgt cgacatttat accgtctgag gtagcagct cgaaactaga 250  
agaagtggag tggccagg gacggcagta tctcttgtg tgaccctggc 300  
ggcctatggg acgtggctt cagaccttg tgatacacca tgctgcgtgg 350  
gacgatgacg gcgtggagag gaatgaggcc tgaggtcaca ctggcttggc 400  
tcctcctagc cacagcaggc tgctttgctg acttgaacga ggtccctcag 450  
gtcaccgtcc agcctgcgtc caccgtccag aagcccggag gcactgtgat 500  
cttgggctgc gtggtaaac ctccaaggat gaatgtaacc tggcgctga 550  
atggaaagga gctgaatggc tcggatgatg ctctgggtgt cctcatcacc 600  
cacgggaccc tcgtcatcac tgcccttaac aaccacactg tggacggta 650  
ccagtgtgtg gcccggatgc ctgcggggc tgtggccagc gtgccagcca 700  
ctgtgacact agccaatctc caggacttca agttagatgt gcagcacgtg 750  
attgaagtgg atgagggaaa cacagcagtc attgcctgcc acctgcctga 800  
gagccacccc aaagcccagg tccggtacag cgtcaaacaa gagtggctgg 850  
aggcctccag aggttaactac ctgatcatgc cctcaggaa cctccagatt 900  
gtgaatgcca gccaggagga cgagggcatg tacaagtgtg cagcctacaa 950  
cccagtgacc caggaagtga aaacctccgg ctccagcgac aggctacgtg 1000  
tgcgccgctc caccgctgag gctgcccga tcatactaccc cccagaggcc 1050  
caaaccatca tcgtcaccaa aggccagagt ctcattctgg agtgtgtggc 1100  
cagtggaaatc ccaccccac ggtcacctg ggccaaggat gggtccagtg 1150  
tcaccggcta caacaagacg cgcttcctgc tgagcaacct cctcatcgac 1200  
accaccagcg aggaggactc aggcacctac cgctgcatgg ccgacaatgg 1250  
ggttggcag cccggggcag cggtcatcct ctacaatgtc caggtgtttg 1300  
aacccccctga ggtcaccatg gagctatccc agctggtcat cccctggggc 1350  
cagagtgcca agcttacctg tgaggtgcgt gggAACCCCC CGCCCTCCGT 1400  
gctgtggctg aggaatgtg tgccctcat ctccagccag cgccctccggc 1450

tctccgcag ggccctgcgc gtgctcagca tggggcctga ggacgaaggc 1500  
gtctaccagt gcatggccga gaacgaggtt gggagcgccc atgccgtagt 1550  
ccagctgcgg acctccaggc caagcataac cccaaggcta tggcaggatg 1600  
ctgagctggc tactggcaca cctcctgtat caccctccaa actcggcaac 1650  
cctgagcaga tgctgagggg gcaaccggcg ctccccagac ccccaacgtc 1700  
agtggggcct gcttccccga agtgtccagg agagaagggg cagggggctc 1750  
ccggcggaggc tcccatcatc ctcagctcgc cccgcacccctc caagacagac 1800  
tcatatgaac tggtgtggcg gcctcggcat gagggcagtg gccggcgcc 1850  
aatcctctac tatgtggtga aacaccgcaa gcaggtcaca aattcctctg 1900  
acgattggac catctctggc attccagcca accagcacccg cctgaccctc 1950  
accagacttg accccgggag cttgtatgaa gtggagatgg cagcttacaa 2000  
ctgtgcggga gagggccaga cagccatggt cacctccga actggacggc 2050  
ggcccaaacc cgagatcatg gccagcaaag agcagcagat ccagagagac 2100  
gaccctggag ccagtcrrca gaggcagcgc cagccagacc acggccgcct 2150  
ctccccccca gaagctcccg acaggccac catctccacg gcctccgaga 2200  
cctcagtgtta cgtgacctgg attccccgtg ggaatggtgg gttcccaatc 2250  
cagtccttcc gtgtggagta caagaagcta aagaaagtgg gagactggat 2300  
tctggccacc agcgccatcc cccatcgcg gctgtccgtg gagatcacgg 2350  
gccttagagaa aggcacctcc tacaagtttc gagtcggg tctgaacatg 2400  
ctgggggaga gcgagcccg cgccccctct cggccctacg tgggtgcggg 2450  
ctacagcggt cgcgtgtacg agaggccgt ggcaggtcct tatatcacct 2500  
tcacggatgc ggtcaatgag accaccatca tgctcaagtg gatgtacatc 2550  
ccagcaagta acaacaacac cccaatccat ggctttata tctattatcg 2600  
acccacagac agtgacaatg atagtgacta caagaaggat atggtgaaag 2650  
gggacaagta ctggcactcc atcagccacc tgcagccaga gacccctac 2700  
gacattaaga tgcagtgcct caatgaagga ggggagagcg agttcagcaa 2750  
cgtgatgatc tgtgagacca aagctcgaa gtcttctggc cagcctggc 2800  
gactgccacc cccaaactctg gccccaccac agccgcccct tcctgaaacc 2850  
atagagcgac cggtgggcac tggggccatg gtggctcgct ccagcgacct 2900

gcctatctg attgtcgaaa tcgtcctggg ctccatcgaa ctcacatcatcg 2950  
tcacccatccc ccccttctgc ttgtggaggg cctggcttaa gcaaaaacat 3000  
acaacagacc tgggtttcc tcgaagtgcc cttccaccct cctgcccgtaa 3050  
tactatggtg ccattgggag gactcccagg ccaccaggcc agtggacagc 3100  
cctacccatcgat tggcatcagt ggacgggcct gtgctaattgg gatccacatg 3150  
aatagggct gcccctcgcc tgcaagtggc tacccggca tgaagccccaa 3200  
gcagcactgc ccaggcgagc ttcagcagca gagtgacacc agcagcctgc 3250  
tgaggcagac ccattttggc aatggatatg acccccaaag tcaccagatc 3300  
acgaggggtc ccaagtcttag cccggacgag ggctcttct tatacacact 3350  
gcccggacgac tccactcacc agctgctgca gccccatcac gactgctgcc 3400  
aacgccagga gcagcctgct gctgtggcc agtcaggggt gaggagagcc 3450  
cccgacagtc ctgtcctgga agcagtgtgg gaccctccat ttcactcagg 3500  
gccccatgc tgcttggcc ttgtgccagt tgaagaggtg gacagtccctg 3550  
actcctgcca agtgagtgga ggagactggt gtccccagca ccccttaggg 3600  
gcctacgtag gacaggaacc tggaatgcag ctctccccgg ggccactggt 3650  
gcgtgtgtct tttgaaacac cacctctcac aatttaggca gaagctgata 3700  
tcccagaaag actatatatt gttttttttt taaaaaaaaa agaagaaaaaa 3750  
agagacagag aaaattggta tttattttc tattatagcc atatttatat 3800  
atttatgcac ttgtaaataa atgtatatgt tttataattc tggagagaca 3850  
taaggagtcc taccctgtga ggttggagag ggaaaataaa gaagctgcca 3900  
cctaacagga gtcacccagg aaagcaccgc acaggctggc gcgggacaga 3950  
ctcctaacct ggggcctctg cagtggcagg cgaggctgca ggaggcccac 4000  
agataagctg gcaagaggaa ggatcccagg cacatggttc atcacgagca 4050  
tgagggaaaca gcaagggca cggtatcaca gcctggagac acccacacag 4100  
atggctggat ccggctgctac gggaaacatt ttcctaagat gcccattgaga 4150  
acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200  
caataatccg tggcaacata tctctgtaaa aacaaacact gtaacttcta 4250  
aataaatgtt tagtcttccc tgtaaaa 4277

<210> 58  
<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

Met	Leu	Arg	Gly	Thr	Met	Thr	Ala	Trp	Arg	Gly	Met	Arg	Pro	Glu
1					5				10					15
Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala
					20				25					30
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr
					35				40					45
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu
					50				55					60
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu
					65				70					75
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr
					80				85					90
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln
					95				100					105
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala
					110				115					120
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln
					125				130					135
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys
					140				145					150
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val
					155				160					165
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met
					170				175					180
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu
					185				190					195
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val
					200				205					210
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr
					215				220					225
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile
					230				235					240
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser
					245				250					255
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser
					260				265					270

Val	Thr	Gly	Tyr	Asn	Lys	Thr	Arg	Phe	Leu	Leu	Ser	Asn	Leu	Leu
				275				280						285
Ile	Asp	Thr	Thr	Ser	Glu	Glu	Asp	Ser	Gly	Thr	Tyr	Arg	Cys	Met
	290				295									300
Ala	Asp	Asn	Gly	Val	Gly	Gln	Pro	Gly	Ala	Ala	Val	Ile	Leu	Tyr
		305				310								315
Asn	Val	Gln	Val	Phe	Glu	Pro	Pro	Glu	Val	Thr	Met	Glu	Leu	Ser
	320			325										330
Gln	Leu	Val	Ile	Pro	Trp	Gly	Gln	Ser	Ala	Lys	Leu	Thr	Cys	Glu
	335				340									345
Val	Arg	Gly	Asn	Pro	Pro	Pro	Ser	Val	Leu	Trp	Leu	Arg	Asn	Ala
	350				355									360
Val	Pro	Leu	Ile	Ser	Ser	Gln	Arg	Leu	Arg	Leu	Ser	Arg	Arg	Ala
	365				370									375
Leu	Arg	Val	Leu	Ser	Met	Gly	Pro	Glu	Asp	Glu	Gly	Val	Tyr	Gln
	380				385									390
Cys	Met	Ala	Glu	Asn	Glu	Val	Gly	Ser	Ala	His	Ala	Val	Val	Gln
	395					400								405
Leu	Arg	Thr	Ser	Arg	Pro	Ser	Ile	Thr	Pro	Arg	Leu	Trp	Gln	Asp
	410					415								420
Ala	Glu	Leu	Ala	Thr	Gly	Thr	Pro	Pro	Val	Ser	Pro	Ser	Lys	Leu
	425					430								435
Gly	Asn	Pro	Glu	Gln	Met	Leu	Arg	Gly	Gln	Pro	Ala	Leu	Pro	Arg
	440					445								450
Pro	Pro	Thr	Ser	Val	Gly	Pro	Ala	Ser	Pro	Lys	Cys	Pro	Gly	Glu
	455					460								465
Lys	Gly	Gln	Gly	Ala	Pro	Ala	Glu	Ala	Pro	Ile	Ile	Leu	Ser	Ser
	470					475								480
Pro	Arg	Thr	Ser	Lys	Thr	Asp	Ser	Tyr	Glu	Leu	Val	Trp	Arg	Pro
	485					490								495
Arg	His	Glu	Gly	Ser	Gly	Arg	Ala	Pro	Ile	Leu	Tyr	Tyr	Val	Val
	500					505								510
Lys	His	Arg	Lys	Gln	Val	Thr	Asn	Ser	Ser	Asp	Asp	Trp	Thr	Ile
	515					520								525
Ser	Gly	Ile	Pro	Ala	Asn	Gln	His	Arg	Leu	Thr	Leu	Thr	Arg	Leu
	530					535								540
Asp	Pro	Gly	Ser	Leu	Tyr	Glu	Val	Glu	Met	Ala	Ala	Tyr	Asn	Cys
	545					550								555
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg

	560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln			
575	580	585	
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp			
590	595	600	
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile			
605	610	615	
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg			
620	625	630	
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys			
635	640	645	
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile			
650	655	660	
Pro Pro Ser Arg Leu Ser Val Glu Ile Thr Gly Leu Glu Lys Gly			
665	670	675	
Thr Ser Tyr Lys Phe Arg Val Arg Ala Leu Asn Met Leu Gly Glu			
680	685	690	
Ser Glu Pro Ser Ala Pro Ser Arg Pro Tyr Val Val Ser Gly Tyr			
695	700	705	
Ser Gly Arg Val Tyr Glu Arg Pro Val Ala Gly Pro Tyr Ile Thr			
710	715	720	
Phe Thr Asp Ala Val Asn Glu Thr Thr Ile Met Leu Lys Trp Met			
725	730	735	
Tyr Ile Pro Ala Ser Asn Asn Asn Thr Pro Ile His Gly Phe Tyr			
740	745	750	
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys			
755	760	765	
Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His			
770	775	780	
Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn			
785	790	795	
Glu Gly Gly Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr			
800	805	810	
Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro			
815	820	825	
Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr Ile Glu Arg			
830	835	840	
Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp Leu Pro			
845	850	855	

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile
					860				865					870
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln
					875				880					885
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro
					890				895					900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His
					905				910					915
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala
					920				925					930
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala
					935				940					945
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu
					950				955					960
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His
					965				970					975
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly
					980				985					990
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro
					995				1000					1005
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys
					1010				1015					1020
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg
					1025				1030					1035
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro
					1040				1045					1050
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu
					1055				1060					1065
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp
					1070				1075					1080
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly
					1085				1090					1095
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr
					1100				1105					1110
Pro	Pro	Leu	Thr	Ile										
					1115									

<210> 59

<211> 25

<212> DNA

<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 59  
gggaaacaca gcagtcattg cctgc 25

<210> 60  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 60  
gcacacgttag cctgtcgctg gagc 24

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-42  
<223> Synthetic construct.

<400> 61  
caccccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62  
<211> 1661  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
cgggaggctg ggtcgcatg atccggaccc cattgtcgcc ctctgccc 50  
cgcctgctcc tcccaggctc ccgcggccga ccccccgcga acatgcagcc 100  
cacgggccgc gagggttccc ggcgcgtcag ccggcggtat ctgcggcg 150  
tgctgctcct gctactgctg ctgctgctgc ggcagccgt aaccgcgcg 200  
gagaccacgc cgggccc cagagccctc tccacgctgg gctcccc 250  
cctcttcaacc acggccgggtg tccccagcgc cctcactacc ccaggcctca 300  
ctacgcccagg caccccaaaa accctggacc ttccgggtcg cgccaggcc 350

ctgatgcgga gtttccact cgtggacggc cacaatgacc tgccccaggt 400  
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450  
tcagccatgg tcagaccaggc ctggacaggc ttagagacgg cctcggtgggt 500  
gcccagttct ggtcagccctc cgtctcatgc cagtcccagg accagactgc 550  
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600  
cctactctga actcgagctt gtgacctcag ctgaaggctt gaacagctct 650  
caaaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700  
cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750  
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800  
agacaccaca tgtacaccaa cgtcagcgga ttgacaagct ttggtgagaa 850  
agtagtagag gagttgaacc gcctggcat gatgataaat ttgtcctatg 900  
catcgacac cttgataaga agggcctgg aagtgtctca ggctcctgtg 950  
atcttctccc actcagctgc cagagctgtg tgtgacaatt tggtaatgt 1000  
tcccgtatgt atcctgcagc ttctgaagaa cggtggcatc gtgatggta 1050  
cactgtccat gggggtgctg cagtcaacc tgcttgctaa cgtgtccact 1100  
gtggcagatc actttgacca catcaggca gtcattggat ctgagttcat 1150  
cgggatttgtt ggaaattatg acgggactgg ccggttccct caggggctgg 1200  
aggatgtgtc cacataccca gtcctgatag aggagttgct gagtcgtasc 1250  
tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300  
cttcagacaa gtggaaaagg tgagagagga gagcaggcg cagagccccg 1350  
tggaggctga gtttccatat gggcaactga gcacatcctg ccactcccac 1400  
ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450  
gccaaccaat cgggtccctt ggaggtcctc aaatgcctcc ccatacctt 1500  
ttccaggcct tgtggctgct gccaccatcc caaccttac ccagtggctc 1550  
tgctgacaca gtcggcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600  
gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650  
cacatggaaa a 1661

<210> 63  
<211> 487  
<212> PRT  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 196, 386  
<223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg
1				5				10					15	
Tyr	Leu	Arg	Arg	Leu	Arg									
				20				25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala
				35				40				45		
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val
				50				55				60		
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro
				65				70				75		
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser
				80				85				90		
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg
				95				100				105		
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe
				110				115				120		
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val
				125				130				135		
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp
				140				145				150		
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His
				155				160				165		
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala
				170				175				180		
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val
				185				190				195		
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser
				200				205				210		
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys
				215				220				225		
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met
				230				235				240		
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val
				245				250				255		
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64  
<211> 25  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.  
  
<400> 64

ccttcacactg cagtacacca tggc 25  
<210> 65  
<211> 25  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.  
  
<400> 65  
gtcacacaca gctctggcag ctgag 25  
  
<210> 66  
<211> 47  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-47  
<223> Synthetic construct.  
  
<400> 66  
ccaagttcag acaccacatg tacaccaacg tcagcgatt gacaaggc 47  
  
<210> 67  
<211> 1564  
<212> DNA  
<213> Homo sapiens  
  
<400> 67  
tgctaggctc tgtcccacaa tgccacccgag agcaggagct gaaaggcctct 50  
aacacccaca gatccctcta tgactgcaat gtgaggtgtc cggtttgct 100  
ggcccagcaa gcctgataag catgaagctc ttatcttgg tggctgtggt 150  
cggtgttttgc tggtgcggc cagctgaagc caacaagagt tctgaagata 200  
tccggtgcaa atgcatttgtt ccaccttata gaaacatcag tggcacatt 250  
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgaa 300  
gcccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgc 350  
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400  
atctacctgt ccgtgggtgg tgccctgttg ctctacatgg ctttcctgat 450  
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500  
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550  
tccctcgaaa gaccccgagc aaacacagtc ctggagcgtg tggaaagggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaaag acagtcttcg 650  
atcgccacaa gatgctcagc tagatggct ggtgtggttt ggtcaaggcc 700  
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750  
ctcccttccc tcggttccag tcttccctt aaaagcctgt ggcattttc 800  
ctccttctcc ctaacttag aaatgttgta cttggctatt ttgattaggg 850  
aagagggatg tggctctga tctctgttgt ctcttgggt ctgggggtt 900  
gaagggaggg ggaaggcagg ccagaaggaa atggagacat tcgaggcggc 950  
ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000  
cagctctgag tcttggaaat gttgttaccc ttggaagata aagctgggtc 1050  
ttcaggaact cagtgtctgg gagaaagca tggccagca ttcatgt 1100  
gttcctttct gcagtggttc ttatcaccac ctccctccca gccccggcgc 1150  
ctcagcccca gccccagctc cagccctgag gacagctctg atggagagc 1200  
tggccccct gagccactg ggtttcagg gtgcactgga agctgggtt 1250  
cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300  
ctctgtgcc ggtccctca cctgcacttg aggggtctgg gcagtccctc 1350  
ctctccccag tgtccacagt cactgagcca gacggtcggt tggaacatga 1400  
gactcgaggc tgagcgtgga tctgaacacc acagccctg tacttgggtt 1450  
gcctcttgc cctgaacttc gttgtaccag tgcatggaga gaaaattttg 1500  
tcctcttgc ttagagttgt gtgtaaatca aggaagccat cattaaattt 1550  
ttttatttct ctca 1564

<210> 68  
<211> 183  
<212> PRT  
<213> Homo sapiens

<400> 68  
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
1 5 10 15  
Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys  
20 25 30  
Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
35 40 45  
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu
				65					70					75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val
				80					85					90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr
				95					100					105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp
				110					115					120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala
				125					130					135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
				140					145					150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys
				155					160					165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys
				170					175					180

Met Leu Ser

<210> 69  
<211> 3170  
<212> DNA  
<213> Homo sapiens

<400> 69  
agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50  
agttcatagg gtcctgggtc cccgaaccag gaagggttga gggAACACAA 100  
tctgcaagcc cccgcgaccc aagtggggg ccccggttg gggtccccc 150  
tcccttgca ttccccacccc tccgggcttt gcgtcttcct gggACCCCC 200  
tcgcgggag atggccgcgt tcatgcggag caaggattcg tcctgctgcc 250  
tgctcctact ggccgcgtg ctgtatgtgg agagctcaca gatcgccagt 300  
tcgcgggcca aactcaactc catcaagtcc tctctggcg gggAGACGCC 350  
tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400  
gcggcagtaa gaaggcAAA aacctgggc aggctaccc tttagcagt 450  
gataaggagt gtgaagtgg gaggtattgc cacagtcccc accaaggatc 500  
atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550  
gcatgtgctg ccccagtacc cgctgcaata atggcatctg tatcccagtt 600  
actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650

cagagatcga aaccacggc attactcaaa ccatgacttg ggatggcaga 700  
atcttaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750  
gaccgcctgcc tacgatcatc agactgcatt gaagggttt gctgtgctcg 800  
tcatttctgg accaaaatct gcaaaccagt gctccatcag gggaaagtct 850  
gtaccaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900  
tgcgactgtg cgaaggccct gtcttgcaaa gtatggaaag atgccaccta 950  
ctccctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000  
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050  
catggtgaa aataagggttc agatgcagaa gaatggctaa aataagaaac 1100  
gtgataagaa tatagatgtat cacaaaaagg gagaaagaaa acatgaactg 1150  
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200  
caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250  
agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300  
aagagtttag gttgtgctgg aggagaggtt tccttcagat tgctgattgc 1350  
ttatacaaataa aacctacatg ccagatttctt attcaacgtt agagtttaac 1400  
aaaatactcc tagaataact tgttatacaa taggttctaa aaataaaaatt 1450  
gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500  
taccccccga tttgtAACAC tacttctgct gttcaatcaa gagtcttgg 1550  
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600  
cagttgttta ggaaggccctt taggaagaca aataaataac aaacaaacag 1650  
ccacaaatac tttttttca aaatttttagt tttacctgta attaataaga 1700  
actgatacaa gacaaaaaca gttcccttcag attctacgga atgacagtat 1750  
atctctcttt atcctatgtg attcctgctc tgaatgcatt atattttcca 1800  
aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850  
ttcacagatg gcaaaaaaaat ttaaagatgt ccaatatatg tggaaaaga 1900  
gctaacagag agatcattat ttcttaaaga ttggccataa cctatatttt 1950  
gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000  
agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050  
aaaactttttt cgtttggca ggtttggca acacatagat catatgtctg 2100

aggcacaagt tggctgttca tctttgaaac cagggatgc acagtctaaa 2150  
tgaatatctg catgggattt gctatcataa tatttactat gcagatgaat 2200  
tcagtgtgag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250  
tgctgagatc ctcaaataat ctcaatttca ggaggttca caaaatgtac 2300  
tcctgaagta gacagagtag tgaggttca ttgccctcta taagcttctg 2350  
actagccaat ggcatcatcc aattttcttc ccaaacctct gcagcatctg 2400  
ctttattgcc aaagggttag tttcggttt ctgcagccat tgcggtaaa 2450  
aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500  
accacagttt ctaaatttctt tgaaaccact ttactacttt ttttaaactt 2550  
aactcagttc taaatacttt gtctggagca caaaacaata aaaggttatc 2600  
ttatagtcgt gactttaaac tttttagac cacaattcac ttttagttt 2650  
tctttactt aaatcccatac tgcagtctca aatttaagtt ctcccagtag 2700  
agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750  
tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800  
caaaaattat aaactagtcc atccaagaac caaagttgt ataaacaggt 2850  
tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttcct 2900  
atataacaat tattatattt acaatttggt ttctgcaata ttttcttat 2950  
gtccaccctt ttaaaaatta ttatttgaag taatttattt acaggaaatg 3000  
ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050  
gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100  
taagataaaa tctattaaat ttttctcctc taaaaactga aaaaaaaaaa 3150  
aaaaaaaaaa aaaaaaaaaa 3170

<210> 70  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 70  
Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu  
1 5 10 15  
Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser  
20 25 30  
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu  
35 40 45

Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly
				50					55				60	
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala
				65					70				75	
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys
				80				85				90		
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg
				95				100				105		
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr
				110				115				120		
Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu
				125				130				135		
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg
				140				145				150		
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu
				155				160				165		
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly
				170				175				180		
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys
				185				190				195		
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln
				200				205				210		
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu
				215				220				225		
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys
				230				235				240		
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val
				245				250				255		
Cys Gln Lys Ile														

<210> 71  
<211> 1809  
<212> DNA  
<213> Homo sapiens

<400> 71  
tctcaatctg ctgacacctgt gatccgcctg accttgtaat ccacacct 50  
tggcctccca aagtgttggg attacaggcg tgagccaccc cgccccggcca 100  
acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150  
cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttt 200

tagtcagttt tcattgcata gtaatatttt catgtagttat tttctaagtt 250  
atattttagt aattcatatg ttttagatta taggtttaa catacttgtg 300  
aaaatacttg atgtgtttta aagccttggg cagaattct gtattgtga 350  
ggatttggtc ttttatcccc cttaaagt catccgtcct tggctcagga 400  
tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450  
tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500  
gtacacagca gaatagtaca agtcacccta caactactac ttcttggac 550  
ctcaagcccc caacatccca gtcctcagtc ctcagtcac ttgacttcaa 600  
atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650  
agcaccagag ccaggcagtc actgttcctc ctccctggtt ggagtccttt 700  
ccttcccagg caaaacttcg agaatcaaca cctggagaca gtcctccac 750  
tgtgaacaag ctttgcagc ttcccagcac gaccattgaa aatatctctg 800  
tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850  
ataccccccag cttctaagat cccagttct gcagtggaaa tgcctgggtc 900  
agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttgggt 950  
cagaaccttc tctctctgaa tttggatcag ctccaagcag tgaaaatagt 1000  
aatcagattc ccatcagctt gtattcgaag tcttaagtg agcctttgaa 1050  
tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100  
ccgtcattac ctccctgcagt ctgacaagct catcaactgaa ttctgctagt 1150  
ccagtagcaa tgtcttcctc ttatgaccag agttctgtgc ataacaggat 1200  
cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250  
tgaatggaca tgggggtggc cgaagtcagc agacactaga cagtaagtat 1300  
agcagcaagc tactcttgc atggctggtg ccaaccaaac agaggaagag 1350  
gatagctcac gtgatgtgga aaacaccagt tggtaatgg ctcattcggt 1400  
aaaaagcagc cctttgcctt tttgtttt ggaccaggtg ttggctgtgg 1450  
tgttattaga aatgtcttaa ccacagcaag aaggagggtgg tggtctcata 1500  
ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagttatgt 1550  
tttaaagatg cttggccag gcgggggtggc tggatgcctt aatcccagtg 1600  
ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctggca acatggtaa actctgtctc tactaaaata cggaaaacta 1700  
gccgggtgtg gtggcgccgc gtgcctgtaa tcccagctac ttgggaggct 1750  
gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800  
ctgaaaaga 1809

<210> 72  
<211> 363  
<212> PRT  
<213> Homo sapiens

<400> 72  
Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile  
1 5 10 15  
Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly  
20 25 30  
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser  
35 40 45  
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr  
50 55 60  
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr  
65 70 75  
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val  
80 85 90  
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val  
95 100 105  
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val  
110 115 120  
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys  
125 130 135  
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys  
140 145 150  
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser  
155 160 165  
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg  
170 175 180  
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro  
185 190 195  
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu  
200 205 210  
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro  
215 220 225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys  
230 235 240

Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala  
245 250 255

Val Gln Asn Ser Thr Tyr Thr Ser Val Ile Thr Ser Cys Ser  
260 265 270

Leu Thr Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser  
275 280 285

Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln  
290 295 300

Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn  
305 310 315

Gly His Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr  
320 325 330

Ser Ser Lys Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg  
335 340 345

Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp  
350 355 360

Leu Ile Arg

<210> 73  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 73  
aattcatggc aaatatttcc cttccc 26

<210> 74  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 74  
tggtaaactg gcccaaactc gg 22

<210> 75  
<211> 50

<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-50  
<223> Synthetic construct

<400> 75  
ttaaagtcat ccgtccttgg ctcaggattt ggagagcttg caccaccaaa 50

<210> 76  
<211> 1989  
<212> DNA  
<213> Homo sapiens

<400> 76  
gcgcgactggg acaaaggcctg gggctggcg gggccatgg cgctgccatc 50  
ccgaatcctg ctttggaaac ttgtgcttct gcagagctct gctgttctcc 100  
tgcactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150  
caccatcaact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200  
caccgacggc ccccccggcca ccccccgccta ctgggacggc gagaaggagg 250  
tgctggcggt ggccgcgcgc gcacccgcgc ttctgacctg cgtgaaccgc 300  
gggcacgtgt ggaccgaccg gcacgtggag gaggctcaac aggtggtgca 350  
ctgggaccgg cagccgccccg gggtcccgca cgaccgcgcg gaccgcctgc 400  
tggacacctata cgcgtcgggc gagcgccgcg cctacggcc ccttttctg 450  
cgccgaccgcg tggctgtggg cgccgatgcc tttgagcgcg gtgacttctc 500  
actgcgtatc gagccgctgg aggtcgccga cgagggcacc tactcctgcc 550  
acctgcacca ccattactgt ggctgcacg aacgcccgcgt cttccacctg 600  
acggtcgccc aaccccacgc ggagccgcgc ccccgggct ctccggcaa 650  
cggtccagc cacagcggcg ccccaggccc agacccaca ctggcgcgcg 700  
gccacacaacgt catcaatgtc atcgccccg agagccgagc ccacttctc 750  
cagcagctgg gctacgtgct ggccacgcgtg ctgctttca tcctgctact 800  
ggtaactgtc ctccctggcg cccgcaggcg cccggaggc tacgaatact 850  
cgaccagaa gtcgggaaag tcaaaggga aggatgttaa cttggcggag 900  
ttcgctgtgg ctgcaggaga ccagatgctt tacaggagtg aggacatcca 950  
gctagattac aaaaacaaca tcctgaagga gagggcggag ctggcccaca 1000  
ccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050

aactgcaaat agggaggccc tgggctcctg gctggccag cagctgcacc 1100  
tctcctgtct gtgctcctcg gggcatctcc tcatgctccg gggctcaccc 1150  
cccttccagc ggctggtccc gcttcctgg aatttggcct gggcgtatgc 1200  
agaggccgcc tccacacccc tccccaggg gcttggtggc agcatagccc 1250  
ccacccctgc ggccttgct cacgggtggc cctgcccacc cctggcacaa 1300  
ccaaaatccc actgatgccc atcatgcct cagacccttc tgggctctgc 1350  
ccgctggggg cctgaagaca ttccctggagg acactcccat cagaacctgg 1400  
cagccccaaa actggggtca gcctcagggc aggagtccca ctccctccagg 1450  
gctctgctcg tccggggctg ggagatgttc ctggaggagg acactcccat 1500  
cagaacttgg cagccttcaa gttggggtca gcctcggcag gagtcccact 1550  
cctcctgggg tgctgcctgc caccaagagc tccccacccat gtaccaccat 1600  
gtgggactcc aggcaccatc tgttctcccc agggacotgc tgacttgaat 1650  
gccagccctt gctcctctgt gttgcttgg gccacctgg gctgcaccc 1700  
ctgcctttc tctgccccat ccctacccta gccttgctct cagccaccc 1750  
gatagtcact gggctccctg tgacttctga ccctgacacc cctcccttgg 1800  
actctgcctg ggctggagtc tagggctggg gctacatttgc gcttctgtac 1850  
tggctgagga caggggaggg agtgaagttg gtttgggtg gcctgtgtt 1900  
ccactctcag caccccacat ttgcattctgc tggtgaccc gacccatca 1950  
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77  
<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 77  
Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu  
1 5 10 15  
Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp  
20 25 30  
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu  
35 40 45  
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro  
50 55 60  
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
65 70 75

Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His
			80					85						90
Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His
			95				100							105
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg
			110					115						120
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro
			125				130							135
Leu	Phe	Leu	Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu
			140				145							150
Arg	Gly	Asp	Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp
			155					160						165
Glu	Gly	Thr	Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu
			170				175							180
His	Glu	Arg	Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala
			185					190						195
Glu	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser
			200				205							210
Gly	Ala	Pro	Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val
			215					220						225
Ile	Asn	Val	Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln
			230				235							240
Leu	Gly	Tyr	Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu
			245				250							255
Val	Thr	Val	Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu
			260				265							270
Tyr	Ser	Asp	Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn
			275				280							285
Leu	Ala	Glu	Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg
			290				295							300
Ser	Glu	Asp	Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu
			305					310						315
Arg	Ala	Glu	Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp
			320				325							330
Leu	Asp	Lys	Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys				
			335				340							

<210> 78  
<211> 2243  
<212> DNA  
<213> Homo sapiens

<400> 78  
cgccggaggc agcggcggcg tggcgcagcg gcgacatggc cggtgtctca 50  
gaggacgact ttcagcacag ttcaaactcc acctacggaa ccacaaggcag 100  
cagtctccga gctgaccagg aggactgt tgagaagctg ctggaccgcc 150  
cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200  
atcttcttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250  
cactgccaag gagtactgga tgttcaaact cccgcaactcc tccagcccag 300  
ccaccgggga ggaccctgag ggctcagaca tcctgaacta ctttgagagc 350  
tacccgtcccg ttgcctccac cgtgccctcc atgctgtgcc tggtgccaa 400  
cttcctgctt gtcaacaggg ttgcagtcca catccgtgtc ctggcctcac 450  
tgacggtcat cctggccatc ttcatggtga taactgcact ggtgaagggtg 500  
gacacttcct cctggacccg tggtttttt gcggtcacca ttgtctgcat 550  
ggtgatcctc agcggtgcct ccactgtctt cagcagcagc atotacggca 600  
tgaccggctc ctttcctatg aggaactccc aagcactgtat atcaggagga 650  
gccatggcg ggacggtcag cgccgtggcc tcattggtgg acttggctgc 700  
atccagtat gtgaggaaca gcgcctggc ctttcctctg acggccacca 750  
tcttcctcgt gctctgcatg ggactctacc tgctgctgtc caggctggag 800  
tatgccaggt actacatgag gcctgttctt gcggcccatg tggttctgg 850  
tgaagaggag cttccccagg actccctcag tgcccattcg gtggcctcca 900  
gattcattga ttccccacaca cccctctcc gccccatctt gaagaagacg 950  
gccagcctgg gcttctgtgt cacctacgtc ttcttcattca ccagcctcat 1000  
ctaccccgcc gtctgcacca acatcgagtc cctcaacaag ggctcgggct 1050  
cactgtggac caccaagttt ttcatcccc tcactacctt cctcctgtac 1100  
aactttgctg acctatgtgg ccggcagctc accgcctgga tccaggtgcc 1150  
agggcccaac agcaaggcgc tcccagggtt cgtgctcctc cggacctgcc 1200  
tcatccccct cttcgtgtc tgtaactacc agccccgcgt ccacctgaag 1250  
actgtggtct tccagtccga tgtgtacccc gcactcctca gctccctgtct 1300  
ggggctcagc aacggctacc tcagcaccct gcccctcctc tacgggccta 1350  
agattgtgcc cagggagctg gctgaggcca cgggagtggt gatgtcctt 1400  
tatgtgtgt tgggcttaac actgggctca gcctgctcta ccctcctgg 1450

gcacctcatc tagaaggag gacacaagga cattgggtct tcagagcctt 1500  
tgaagatgag aagagagtgc aggaggcgtg gggccatgg agaaaggcc 1550  
taaagttca cttgggaca gagagcagag cacactcggt cctcatccct 1600  
ccaaagatgc cagtggcca cgtccatgcc cattccgtgc aaggcagata 1650  
ttccagtcat attaacagaa cactcctgag acagttgaag aagaaatagc 1700  
acaaatcagg ggtactccct tcacagctga tggtaacat tccacccct 1750  
ttcttagccct tcaaagatgc tgccagtggtt cgccctagag ttattacaaa 1800  
gccagtgcca aaacccagcc atgggctt tgcaacccctc cagctgcgt 1850  
cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttaccct 1900  
gaaggggtct ccctggaatg gaagtcccct ggcatggtca gtcctcaggc 1950  
ccaagactca agtgtgcaca gaccctgtg ttctgcgggt gaacaactgc 2000  
ccactaacca gactggaaaa cccagaaaga tggccttcc atgaatgctt 2050  
cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100  
ggcctgggtt ttcaaaaaaaaaa gagggatcct catgacctgg tggcttatgg 2150  
cctgggtcaa gatgagggtc tttcagtggtt cctgtttaca acatgtcaaa 2200  
gccattgggtt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser
1				5				10					15	

Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	
				20			25					30		

Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg
			35			40						45		

Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu
			50					55					60	

Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys
			65					70					75	

Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr
			80				85					90		

Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser
			95						100				105	

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val  
 110 115 120  
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val  
 125 130 135  
 Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr  
 140 145 150  
 Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe  
 155 160 165  
 Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr  
 170 175 180  
 Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met  
 185 190 195  
 Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr  
 200 205 210  
 Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp  
 215 220 225  
 Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe  
 230 235 240  
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu  
 245 250 255  
 Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe  
 260 265 270  
 Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser  
 275 280 285  
 Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro  
 290 295 300  
 Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val  
 305 310 315  
 Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile  
 320 325 330  
 Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe  
 335 340 345  
 Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu  
 350 355 360  
 Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn  
 365 370 375  
 Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile  
 380 385 390  
 Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser		
410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu		
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly		
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser		
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu Ile		
470	475	

<210> 80

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 80

ttttgcggtc accattgtct gc 22

<210> 81

<211> 23

<212> DNA

<213> Homo sapiens

<220>

<221> Artificial sequence

<222> 1-23

<223> Synthetic construct.

<400> 81

cgttaggtgac acagaagccc agg 23

<210> 82

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-49

<223> Synthetic construct.

<400> 82

tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83

<211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

gacagtggag ggcagtggag aggaccgcgc tgtcctgctg tcaccaagag 50  
ctggagacac catctccac cgagagtcat ggccccattg gccctgcacc 100  
tcctcgctt cgtccccatc ctcctcagcc tggtgtgcctc ccaggactgg 150  
aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200  
ctatgagcag ctgctcaagg tggtgacctg ggggctcaat cggaccctga 250  
agccccagag ggtgattgtg gttggcgctg gtgtggccgg gctggtgccc 300  
gccaaagggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350  
taacaggatc gggggccgca tttcaccta ccgggaccag aacacgggct 400  
ggattgggaa gctgggagcc atgcgcattgc ccagctctca caggatcctc 450  
cacaagctct gccaggccct gggctcaac ctgaccaagt tcacccagta 500  
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550  
tggtgagaa ggtgcccggag aagctggct acgccttgcg tccccagggaa 600  
aaggggccact cgccccgaaga catctaccag atggctotca accaggccct 650  
caaagacctc aaggcactgg gctgcagaaa ggcgatgaag aagtttgaaa 700  
ggcacacgct cttggatat cttctcgggg aggggaacct gagccggccg 750  
gccgtgcagc ttctgggaga cgtatgtcc gaggatggct tcttctatct 800  
cagcttcgccc gaggccctcc gggcccacag ctgcctcagc gacagactcc 850  
agtacagccg catcgtgggt ggctggacc tgctgcccg cgcgctgctg 900  
agctcgctgt ccgggcttgt gctgttgaac ggcggctgg tggcgatgac 950  
ccagggaccg cacgatgtgc acgtgcagat cgagacctct ccccccggcgc 1000  
ggaatctgaa ggtgctgaag gccgacgtgg tgctgctgac ggcgagcgg 1050  
ccggcggtga agcgcatcac cttctcgccg ccgctgcccc gccacatgca 1100  
ggaggcgctg cggaggctgc actacgtgcc ggccaccaag gtgttcctaa 1150  
gcttccgcag gcccttctgg cgcgaggagc acattgaagg cggccactca 1200  
aacaccgatc gcccgtcgcg catgattttc tacccgcgcg cgcgcgagg 1250  
cgcgctgctg ctggcctcgat acacgtggtc ggacgcggcg gcagcgatcg 1300  
ccggcttgag ccgggaagag gcgttgcgt tggcgctcga cgacgtggcg 1350

gcattgcacg ggcctgtcgt gcgccagctc tgggacggca cccggcgtcgt 1400  
caagcggttgg gcggaggacc agcacagcca gggtgtttt gtggtagc 1450  
cgccggcgct ctggcaaacc gaaaaggatg actggacggt cccttatggc 1500  
cgcatctact ttgcccggcga gcacaccgccc tacccgcacg gctgggtgga 1550  
gacggcggtc aagtccggcgc tgccgcgc catcaagatc aacagccgga 1600  
aggggcctgc atcggacacg gccagccccg aggggcacgc atctgacatg 1650  
gaggggcagg ggcatgtgca tgggtggcc agcagccct cgcatgaccc 1700  
ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750  
aaaacacgac ccacacgagg acctcgcatt aaagtatttt cgaaaaaaa 1800  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu
1									10					15
Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln
									25					30
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu
						35			40					45
Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln
						50			55					60
Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala
					65				70					75
Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala
					80				85					90
Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn
						95			100					105
Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser
						110			115					120
His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu
						125			130					135
Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His
						140			145					150
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys
						155			160					165

Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu  
 170 175 180  
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys  
 185 190 195  
 Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr  
 200 205 210  
 Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala  
 215 220 225  
 Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr  
 230 235 240  
 Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp  
 245 250 255  
 Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro  
 260 265 270  
 Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala  
 275 280 285  
 Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln  
 290 295 300  
 Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala  
 305 310 315  
 Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile  
 320 325 330  
 Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg  
 335 340 345  
 Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg  
 350 355 360  
 Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn  
 365 370 375  
 Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu  
 380 385 390  
 Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala  
 395 400 405  
 Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu  
 410 415 420  
 Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp  
 425 430 435  
 Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser  
 440 445 450  
 Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
 ctgacatggc ctgactcgaa acagctcaga gcagggcaga actggggaca 50  
 ctctgggccg gccttctgcc tgcattggacg ctctgaagcc accctgtctc 100  
 tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150  
 gaactcagag ccgggaagcc cccattcaact agaagcactg agagatgcgg 200  
 ccccctcgca gggctgaat ttccctgctgc tgttcacaaa gatgcttttt 250  
 atcttaact ttttgttttc cccacttccg accccggcgt tgatctgcat 300  
 cctgacattt ggagctgcca tcttcttgta gctgatcacc agacctcaac 350  
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggaa 400  
 ggagcacgga aggggtttc ccagaagaac aatgaccta caagttgctg 450  
 cttctcagat gccaagacta tgtatgaggt tttccaaaga ggactcgctg 500  
 tgtctgacaa tggccctgc ttggatata gaaaacaaaa ccagccctac 550  
 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600  
 ctgtctcttg cataaagggtt ataaatcatc accagaccag tttgtcggca 650  
 tctttgctca gaataggcca gagtggatca tctccgaatt ggcttggtac 700  
 acgtactcta tggtagctgt acctctgtat gacacccctgg gaccagaagc 750

catcgatcat attgtcaaca aggctgatat cgccatggtg atctgtgaca 800  
caccccaaaa ggcattggtg ctgataggaa atgtagagaa aggcttcacc 850  
ccgagcctga aggtgatcat ctttatggac ccctttagatg atgacctgaa 900  
gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgctg 950  
agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000  
gacctgagcg tcatactgctt caccagtggg accacaggtg accccaaagg 1050  
agccatgata acccatcaaa atattgttcc aaatgctgct gccttctca 1100  
aatgtgtgga gcatgcttat gagccactc ctgatgatgt gccatatacc 1150  
taccccttc tggctcatat gttttagagg attgtacagg ctgtgtgt 1200  
cagctgtgga gccagagttg gattcttcca agggatatt cggttgctgg 1250  
ctgacgacat gaagactttg aagccacat ttttccgc ggtgcctcga 1300  
ctcccttaaca ggtatctacga taaggtacaa aatgaggcca agacaccctt 1350  
gaagaagttc ttgttgaagc tggctgttcc cagtaaattc aaagagcttc 1400  
aaaagggtat catcaggcat gatagtttct gggacaagct catcttgca 1450  
aagatccagg acagcctggg cggaagggtt cgttaattt tcactggagc 1500  
tgccccatg tccacttcag tcatgacatt cttccggca gcaatggat 1550  
gtcaggtgta tgaagcttat ggtcaaacag aatgcacagg tggctgtaca 1600  
tttacattac ctggggactg gacatcaggt cacgttgggg tgccctggc 1650  
ttgcaattac gtgaagctgg aagatgtggc tgacatgaac tactttacag 1700  
tgaataatga aggagaggc tgcataagg gtacaaacgt gttcaaaagga 1750  
tacctgaagg accctgagaa gacacaggaa gccctggaca gtgatggctg 1800  
gcttcacaca ggagacattt gtcgctggct cccgaatgga actctgaaga 1850  
tcatcgaccg taaaaagaac attttcaagc tggcccaagg agaatacatt 1900  
gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950  
aattttgtt cacggggaga gcttacggc atccttagta ggagtgggtgg 2000  
ttcctgacac agatgtactt ccctcattt cagccaagct tgggtgtt 2050  
ggctcctttg aggaactgtg ccaaaaccaa gttgttaaggg aagccatttt 2100  
agaagacttg cagaaaattt gaaagaaag tggccttaaa acttttgaac 2150  
aggtaaaaggc cattttctt catccagagc catttccat tgaaaatggg 2200

ctcttgacac caacattgaa agcaaagcga ggagagctt ccaaatactt 2250  
tcggacccaa attgacagcc tgtatgagca catccaggat taggataagg 2300  
tacttaagta cctgccggcc cactgtcac tgcttgtag aaaaatggatt 2350  
aaaaaactatt ctacatttg ttttgcctt cctcctatTT ttttttaacc 2400  
tgttaaactc taaagccata gctttgttt tatattgaga catataatgt 2450  
gtaaacttag ttcccaaata aatcaatcct gtcttccc tcttcgatgt 2500  
tgctaataatt aaggcttcag ggctactttt atcaacatgc ctgtcttcaa 2550  
gatcccagtt tatgttctgt gtccttcctc atgatttcca accttaatac 2600  
tattagtaac cacaagttca agggtcaaag ggaccctctg tgccttcttc 2650  
tttgggggt gataaacata acttgccaac agtctctatg cttatTTaca 2700  
tcttctactg ttcaaactaa gagattttta aattctgaaa aactgcttac 2750  
aattcatgtt ttctagccac tccacaaacc actaaaattt tagttttagc 2800  
ctatcactca tgtcaatcat atctatgaga caaatgtctc cgatgcttt 2850  
ctgcgtaaat taaattgtgt actgaaggga aaagtttgat cataccaaac 2900  
atTCCTAAA ctctctagtt agatatctga cttgggagta ttAAAAATTG 2950  
ggtctatgac atactgtcca aaaggaatgc tggcttAAA gcattattta 3000  
cagtaggaac tggggagtaa atctgttccc tacagttgc tgctgagctg 3050  
gaagctgtgg gggaggagt tgacaggtgg gcccagtgaa cttttccagt 3100  
aaatgaagca agcactgaat aaaaacctcc tgaactggga acaaagatct 3150  
acaggcaagc aagatgcccacaacacaggc ttatTTCTG tgaaggaacc 3200  
aactgatctc cccccaccctt ggatttagagt tcctgctcta ctttacccac 3250  
agataacaca tgggtttct acttgtaat gtaaagtctt taaaataaac 3300  
tattacagat aaaaaa 3316

<210> 86  
<211> 739  
<212> PRT  
<213> Homo sapiens

<400> 86  
Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg  
1 5 10 15  
Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro  
20 25 30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser
				35					40				45	
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile
				50					55			60		
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys
				65					70			75		
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg
				80					85			90		
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val
				95					100			105		
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn
				110					115			120		
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu
				125					130			135		
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu
				140					145			150		
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys
				155					160			165		
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His
				170					175			180		
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala
				185					190			195		
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr
				200					205			210		
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu
				215					220			225		
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile
				230					235			240		
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu
				245					250			255		
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro
				260					265			270		
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu
				275					280			285		
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe
				290					295			300		
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys
				305					310			315		
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr

	320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val			
335	340	345	
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr			
350	355	360	
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val			
365	370	375	
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg			
380	385	390	
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro			
395	400	405	
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn			
410	415	420	
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val			
425	430	435	
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp			
440	445	450	
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu			
455	460	465	
Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser			
470	475	480	
Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val			
485	490	495	
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe			
500	505	510	
Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu			
515	520	525	
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr			
530	535	540	
Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn			
545	550	555	
Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala			
560	565	570	
Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp			
575	580	585	
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile			
590	595	600	
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu			
605	610	615	

Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His  
620 625 630

Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp  
635 640 645

Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly  
650 655 660

Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile  
665 670 675

Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr  
680 685 690

Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser  
695 700 705

Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly  
710 715 720

Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu  
725 730 735

His Ile Gln Asp

<210> 87

<211> 2725

<212> DNA

<213> Homo sapiens

<400> 87

ggaggcggag gccgcggcga gccgggcccga gcagtggaggg ccctagcg 50  
gcccgagcgg ggccccggggc ccctaagcca ttccctgaagt catgggctgg 100  
ccaggacatt ggtgaccgc caatccggta tggacgactg gaagcccagc 150  
cccctcatca agccctttgg ggctcggaaag aagcggagct ggtaccttac 200  
cttggaaatataaaactgaccaa accagcgggc cctgcggaga ttctgtcaga 250  
caggggccgt gctttcctg ctggtgactg tcattgtcaa tatcaagttg 300  
atccctggaca ctcggcgagc catcagtgaa gccaatgaag acccagagcc 350  
agagcaagac tatgtatgagg ccctaggccg cctggagccc ccacggcgca 400  
gaggcagtgg tccccggcgg gtcctggacg tagaggtgta ttcaagtcgc 450  
agcaaagtat atgtggcagt ggtggcacc acggtgctgg aggatgaggc 500  
ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550  
gccacgtgat ggcaaaaacgt gtgtttgaca cgtactcacc tcatgaggat 600  
gaggccatgg tgctattcct caacatggta gcgcccgcc gagtgctcat 650

ctgcactgtc aaggatgagg gtccttcca cctcaaggac acagccaagg 700  
ctctgcttag gagcctgggc agccaggctg gccctgcctt gggctggagg 750  
gacacatggg cttcgtgg acgaaaagga ggtcctgtct tcggggagaa 800  
acattctaag tcacctgccc tctttcctg gggggaccca gtcctgctga 850  
agacagatgt gccattgagc tcagcagaag aggtagtg ccactggca 900  
gacacagagc tgaaccgtcg ccgcggcgc ttctgcagca aagttgaggg 950  
ctatgaaat gtatgcagct gcaaggaccc cacacccatc gagttcagcc 1000  
ctgacccact cccagacaac aaggcctca atgtgcctgt ggctgtcatt 1050  
gcagggAACc gaccaatta cctgtacagg atgctgcgt ctctgcttc 1100  
agcccagggg gtgtctcctc agatgataac agttttcatt gagggctact 1150  
atgaggaacc catggatgtg gtggcactgt ttggcttgag gggcatccag 1200  
catactccca tcagcatcaa gaatgccgc gtgtctcagc actacaaggc 1250  
cagcctcaact gccactttca acctgtttcc ggaggccaag tttgtgtgg 1300  
ttctgaaaga ggacctggac attgctgtgg attttttcag tttctgagc 1350  
caatccatcc acctacttggaa ggaggatgac agcctgtact gcatctctgc 1400  
ctggaatgac caggggtatg aacacacggc tgaggaccca gcactactgt 1450  
accgtgttggaa gaccatgcct gggctggct gggctgtcag gaggtccttg 1500  
tacaaggagg agcttgcgttca caagtggcctt acaccggaaa agctctggaa 1550  
ttgggacatg tggatgcgga tgcctgaaca acgccccggc cgagagtgc 1600  
tcatccctga cgtttcccgaa tccttaccact ttggcatgtt cggcctcaac 1650  
atgaatggct actttcacgtt ggcctacttc aagaagcaca agttcaacac 1700  
ggttccaggt gtccagctca ggaatgttggaa cagtctgaag aaagaagctt 1750  
atgaagtggaa agttcacagg ctgctcagtg aggctgaggt tctggaccac 1800  
agcaagaacc cttgtgaaga ctctttcctg ccagacacag agggccacac 1850  
ctacgtggcc ttatttcgaa tggagaaaga tggacttc accacctggaa 1900  
cccagcttgc caagtgcctc cttatctggg acctggatgtt gctggcaac 1950  
catcggggcc tggagattt gtttcggaaag aagaaccactt tcctgggtt 2000  
gggggtcccg gcttccccctt actcagtggaa gaagccaccc tcagtcaccc 2050  
caatttccctt ggagccaccc ccaaaggagg agggagcccc aggagccca 2100

gaacagacat gagacccctt ccaggaccct gcggggctgg gtactgtgta 2150  
cccccaggct ggcttagccct tccctccatc ctgttaggatt ttgttagatgc 2200  
tggtagggc tggggctacc ttgttttaa catgagactt aattactaac 2250  
tccaagggga gggttccctt gctccaacac cccgttcctg agttaaaagt 2300  
ctatttattt acttccttgt tggagaaggg caggagagta cctggaaatc 2350  
attacgatcc ctagcagctc atcctgccct ttgaataaccc tcactttcca 2400  
ggcctggctc agaatctaac ctatttattt actgtcctga gggccttgaa 2450  
aacaggccga acctggaggg cctggatttc ttttgggct ggaatgctgc 2500  
cctgagggtg gggctggctc ttactcagga aactgctgtg cccaacccat 2550  
ggacaggccc agctggggcc cacatgctga cacagactca ctcagagacc 2600  
cttagacact ggaccaggcc tcctctcagc cttctcttg tccagatttc 2650  
caaagctgga taagttggtc attgattaaa aaaggagaag ccctctggga 2700  
aaaaaaaaaaaaaaa aaaaaaa 2725

<210> 88  
<211> 660  
<212> PRT  
<213> Homo sapiens

<400> 88  
Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala  
1 5 10 15  
Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr  
20 25 30  
Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu  
35 40 45  
Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp  
50 55 60  
Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu  
65 70 75  
Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
80 85 90  
Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
95 100 105  
Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu  
110 115 120  
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val  
125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp  
                  140                 145                 150  
 Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn  
                  155                 160                 165  
 Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu  
                  170                 175                 180  
 Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser  
                  185                 190                 195  
 Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp  
                  200                 205                 210  
 Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His  
                  215                 220                 225  
 Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu  
                  230                 235                 240  
 Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His  
                  245                 250                 255  
 Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser  
                  260                 265                 270  
 Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr  
                  275                 280                 285  
 Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu  
                  290                 295                 300  
 Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu  
                  305                 310                 315  
 Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro  
                  320                 325                 330  
 Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met  
                  335                 340                 345  
 Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro  
                  350                 355                 360  
 Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser  
                  365                 370                 375  
 Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val  
                  380                 385                 390  
 Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe  
                  395                 400                 405  
 Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr  
                  410                 415                 420  
 Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly		
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys		
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg		
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val		
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu		
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr		
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp		
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu		
635	640	645
Pro Pro Pro Lys Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr		
650	655	660

<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgttg acacg 25

<210> 90  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 90  
cctcaaccag gccacgggcc ac 22

<210> 91  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 91  
cccaggcaga gatgcagtagc aggc 24

<210> 92  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 92  
cctccagtag gtggatggat tggctc 26

<210> 93  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 93  
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94  
<211> 3037  
<212> DNA  
<213> Homo sapiens

<400> 94

cggaacgcgtg ggctgctgg gggaaaggcct aaagaactgg aaagcccaact 50  
ctcttggAAC caccacacct gtttaaAGAA cctaAGCACC atttaaAGCC 100  
actggAAatt tttgtctAG tgggtgtGGG tgaataaAGG agggcagaat 150  
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgGGat 200  
gttacgtggc cggaatcatt cccttggctg ttaatttctc agaggaacga 250  
ctgaagctgg tgactgtttt gggtgctggc cttctctgtg gaactgctct 300  
ggcagtcATC gtgcctGAAG gagtACATGC cctttatGAA gatattcttG 350  
agggAAAACA ccaccaAGCA agtGAAACAC ataAtgtGAT tgcAtcAGAC 400  
aaAGcAGcAG aaaaAtcAGT tgcAtGAA catGAGcACA gCcAcGACCA 450  
cacacAGctg catgcCTATA ttggtgTTtC cctcgTTctG ggcttcgttt 500  
tcatgttGtC ggtggaccAG attggtaACT cccatgtGCA ttctactGAC 550  
gatccagaAG cagcaAGGTC tagcaATTCC aaaAtcACCA ccacGCTGGG 600  
tctggttGtC catgctGcAG ctgatggtGt tgctttGGGA gcAGcAGcAt 650  
ctacttcaca gaccAGtGtC cagttAAttG tggGGtGtGc aatcatGctA 700  
cataaggcac cagctgCTtT tggactggTT tccttcttGA tgoAtGtGg 750  
cttagagcgg aatcgaatca gaaAGcACTt gctggtCTtT gcattGGcAG 800  
caccAGttt gtccatggtG acatacttag gactgAGtAA gagcAGtAAA 850  
gaagcccTTT cagaggGTGAA cgccAcGGGA gtggccATGC ttttctctGc 900  
cgggacATTt ctTTatGTTG ccacAGtACA tgcTcTCCtT gaggtGGGcG 950  
gaatAGGGca cagccacaAG cccGAtGCCA cgggaggGGAG aggCCTcAGC 1000  
cgccTggAAAG tggcAGcCCT ggTTctGGGT tgcctcatCC ctctcatCCT 1050  
gtcAGtagGA caccAGcATT aaAtgttCAA ggtccAGcCT tggTccAGGG 1100  
ccgTTGcca tccAGtGAGA acagccGGca cgtGACAGcT actcacttCC 1150  
tcagtctctt gtctcacCTt gcgcAtctcT acatgtattc ctAgAGtCCA 1200  
gaggGGAGGT gaggttAAAA cctgAGtAAt ggAAAGcTT ttagAGtAGA 1250  
aacacatttA cgttgcAGtT agctAtAGAC atcccattGT gttatctttt 1300  
aaaaggccCT tgacattttG cgTTtaATA ttTctcttAA ccctattCTC 1350  
agggAAAGAtG gaatttagtt ttaAGGAAA gaggAGAact tcataCTcAC 1400  
aatgAAAAtAG tgattatGAA aatacAGtGT tctgtAAAtTA agctatgtct 1450

cTTTCTTCTT agtttagagg ctctgctact ttatccattt atttttaaca 1500  
tggTTcccac catgtaagac tggtgcttta gcatctatgc cacatgcgtt 1550  
gatggaaggt catagcaccc actcacttag atgctaaagg tgattctagt 1600  
taatctggta ttagggtcag gaaaatgata gcaagacaca ttgaaagctc 1650  
tctttatact caaaagagat atccattgaa aaggatgtc tagagggatt 1700  
taaacagctc ctttggcacg tgccctcttg aatccagcct gccattccat 1750  
caaatggagc aggagaggtg ggaggagctt ctaaagaggt gactggatt 1800  
ttgttagcatt ctttgtcaag ttctcctttt cagaataacct gtctccacat 1850  
tccttagagag gagccaagtt ctagtagttt cagttctagg ctttccttca 1900  
agaacagtca gatcacaaag tgtctttgga aattaaggga tattaaattt 1950  
taagtgattt ttggatggtt attgatatct ttgttagtagc tttttttaaa 2000  
agactaccaa aatgtatggt tgccctttt ttttgtttt tttttttta 2050  
attatttctc ttagcagatc agcaatccct ctagggacct aaatactagg 2100  
tcagctttgg cgacactgtg tcttcacca taaccacctg tagcaagatg 2150  
gatcataaat gagaagtgtt tgccatttga tttaaagctt attgaaatca 2200  
tgtctcttgt ctcttcgtct tttcttgct tttcttctaa cttttccctc 2250  
tagcctctcc tcgccacaat ttgctgctta ctgctggtgt taatatttgt 2300  
gtgggatgaa ttcttatcag gacaaccact tctcgaaactg taataatgaa 2350  
gataataata tctttattct ttatcccctt caaagaaatt acctttgtgt 2400  
caaatgccgc tttgttgagc cctaaaata ccacccctc atgtgtaaat 2450  
tgacacaatc actaatctgg taatttaaac aattgagata gcaaaagtgt 2500  
ttaacagact aggataattt tttttcata tttgccaaaa tttttgtaaa 2550  
ccctgtcttg tcaaataagt gtataatatt gtattattaa ttttatttta 2600  
ctttctatac catttcaaaa cacattacac taagggggaa ccaagactag 2650  
tttcttcagg gcagtggacg tagtagtttga taaaacgtt ttctatgacg 2700  
cataagctag catgcctatg atttatttcc ttcatgaatt tgtcactgga 2750  
tcagcagctg tggaaataaa gcttgtgagc cctctgctgg ccacagttag 2800  
gaaagtagca caaataggat acagttgtat gtagtcattt gcaacaattt 2850  
cataacaattt tactaccaag agaaggtata gtatggaaag tccaaatgac 2900

ttccttgatt ggatgttaac agctgactgg tgtgagactt gaggtttcat 2950  
ctagtccttc aaaactataat ggtgcctag attctctctg gaaactgact 3000  
ttgtcaaata aatagcagat ttagtgtca aaaaaaa 3037

<210> 95  
<211> 307  
<212> PRT  
<213> Homo sapiens

<400> 95  
Met Asp Asp Phe Ile Ser Ile Ser Leu Leu Ser Leu Ala Met Leu  
1 5 10 15  
Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe  
20 25 30  
Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu  
35 40 45  
Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His  
50 55 60  
Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser  
65 70 75  
Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser  
80 85 90  
Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His  
95 100 105  
Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu  
110 115 120  
Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp  
125 130 135  
Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu  
140 145 150  
Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala  
155 160 165  
Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val  
170 175 180  
Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser  
185 190 195  
Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His  
200 205 210  
Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr  
215 220 225  
Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

	230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu			
245	250	255	
Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly			
260	265	270	
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg			
275	280	285	
Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile			
290	295	300	
Leu Ser Val Gly His Gln His			
305			

<210> 96

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 96

gttgtgggtg aataaaggag ggcag 25

<210> 97

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 97

ctgtgctcat gttcatggac aactg 25

<210> 98

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-50

<223> Synthetic construct.

<400> 98

ggatgatttc atctccatTA gcctgctgtc tctggctatg ttgggtggat 50

<210> 99

<211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

gctcgaggcc ggcggcggcg ggagagcgac ccgggcggcc tcgttagcggg 50  
gcccccggatc cccgagtggc ggccggagcc tcgaaaagag attctcagcg 100  
ctgattttga gatgatgggc ttggaaacg ggcgtcgcag catgaagtcg 150  
ccgccccctcg tgctggccgc cctgggtggcc tgcacatcatcg tcttgggctt 200  
caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250  
tggagctgga aggcagggtc cgcaaggcgg ctgcagagag aggccgcgtg 300  
gagctgaaga agaacgagtt ccagggagag ctggagaagc agcgggagca 350  
gcttgacaaa atccagtcga gccacaactt ccagctggag agcgtcaaca 400  
agctgtacca ggacgaaaag gcgggtttgg tgaataacat caccacaggt 450  
gagaggctca tccgagtgtc gcaagaccag ttaaagaccc tgcagaggaa 500  
ttacggcagg ctgcagcagg atgcctcca gtttcagaag aaccagacca 550  
acctggagag gaagttctcc tacgacctga gccagtgcattt caatcagatg 600  
aaggaggtga aggaacagtg tgaggagcga atagaagagg tcaccaaaaa 650  
ggggaatgaa gctgttagctt ccagagacct gagtgaaaac aacgaccaga 700  
gacagcagct ccaagccctc agtgagcctc agcccaggct gcaggcagca 750  
ggcctgccac acacagaggt gccacaaggg aaggaaacg tgcttggtaa 800  
cagcaagtcc cagacaccag cccccagtcc cgaagtggtt ttggattcaa 850  
agagacaagt tgagaaaagag gaaaccaatg agatccaggt ggtgaatgag 900  
gagcctcaga gggacaggct gccgcaggag ccaggccggg agcaggtgg 950  
ggaagacaga cctgttaggtg gaagaggctt cgggggagcc ggagaactgg 1000  
gccagacccc acaggtgcag gctgccctgt cagtgagcca ggaaaatcca 1050  
gagatggagg gccctgagcg agaccagctt gtcattccccg acggacagga 1100  
ggaggagcag gaagctgccg gggaaaggag aaaccagcag aaactgagag 1150  
gagaagatga ctacaacatg gatgaaaatg aagcagaatc tgagacagac 1200  
aagcaagcag ccctggcagg gaatgacaga aacatagatg ttttaatgt 1250  
tgaagatcag aaaagagaca ccataaattt acttgatcag cgtaaaaagc 1300  
ggaatcatac actctgaatt gaactggaat cacatattc acaacaggc 1350

cgaagagatg actataaaat gttcatgagg gactgaatac taaaaactgt 1400  
gaaatgtact aaataaaaatg tacatctga 1429

<210> 100  
<211> 401  
<212> PRT  
<213> Homo sapiens

<400> 100  
Met Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro  
1 5 10 15  
Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe  
20 25 30  
Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg  
35 40 45  
Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg  
50 55 60  
Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu  
65 70 75  
Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe  
80 85 90  
Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val  
95 100 105  
Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu  
110 115 120  
Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln  
125 130 135  
Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg  
140 145 150  
Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu  
155 160 165  
Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys  
170 175 180  
Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp  
185 190 195  
Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu  
200 205 210  
Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly  
215 220 225  
Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser  
230 235 240

Glu	Val	Val	Leu	Asp	Ser	Lys	Arg	Gln	Val	Glu	Lys	Glu	Glu	Thr
														255
				245							250			
Asn	Glu	Ile	Gln	Val	Val	Asn	Glu	Glu	Pro	Gln	Arg	Asp	Arg	Leu
														270
				260						265				
Pro	Gln	Glu	Pro	Gly	Arg	Glu	Gln	Val	Val	Glu	Asp	Arg	Pro	Val
														285
				275						280				
Gly	Gly	Arg	Gly	Phe	Gly	Gly	Ala	Gly	Glu	Leu	Gly	Gln	Thr	Pro
														300
				290						295				
Gln	Val	Gln	Ala	Ala	Leu	Ser	Val	Ser	Gln	Glu	Asn	Pro	Glu	Met
														315
				305						310				
Glu	Gly	Pro	Glu	Arg	Asp	Gln	Leu	Val	Ile	Pro	Asp	Gly	Gln	Glu
														330
				320						325				
Glu	Glu	Gln	Glu	Ala	Ala	Gly	Glu	Gly	Arg	Asn	Gln	Gln	Lys	Leu
														345
				335						340				
Arg	Gly	Glu	Asp	Asp	Tyr	Asn	Met	Asp	Glu	Asn	Glu	Ala	Glu	Ser
														360
				350						355				
Glu	Thr	Asp	Lys	Gln	Ala	Ala	Leu	Ala	Gly	Asn	Asp	Arg	Asn	Ile
														375
				365						370				
Asp	Val	Phe	Asn	Val	Glu	Asp	Gln	Lys	Arg	Asp	Thr	Ile	Asn	Leu
														390
				380						385				
Leu	Asp	Gln	Arg	Glu	Lys	Arg	Asn	His	Thr	Leu				
				395						400				

```
<210> 101
<211> 3671
<212> DNA
<213> Homo sapiens

<400> 101
ggatgcagaa agcctcagtg ttgctcttcc tggcctgggt ctgcttcctc 50
ttctacgctg gcattgccct cttcaccagt ggcttcctgc tcacccgttt 100
ggagctcacc aaccatagca gctgccaaga gcccccaggc cctgggtccc 150
tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccga 200
tttgcggg ttgtgttgtt gctgatagat gctctgcgtt ttgacttcgc 250
ccagccccag cattcacacg tgccttagaga gccttcgttc tccctaccct 300
tcctggcaa actaagctcc ttgcagagga tcctggagat tcagccccac 350
catgccccggc tctaccgatc tcaggttgac cctcctacca ccaccatgca 400
gcgcctcaag gccctcacca ctggctcaact gcctacctt attgatgctg 450
gtagtaacctt cgccagccac gccatagtgaa aagacaatct cattaagcag 500
```

ctcaccagtg caggaaggcg tgttagtcttc atgggagatg atacctggaa 550  
agacctttc cctggtgctt tctccaaagc tttcttcttc ccatccttca 600  
atgtcagaga cctagacaca gtggacaatg gcatcctgga acacctctac 650  
cccaccatgg acagtggtga atgggacgtg ctgattgctc acttcctggg 700  
tgtggaccac tgtggccaca agcatggccc tcaccaccct gaaatggcca 750  
agaaaacttag ccagatggac caggtgatcc agggacttgt ggagcgtctg 800  
gagaatgaca cactgcttgt agtggctgg gaccatggga tgaccacaaa 850  
tggagaccat ggaggggaca gtgagctgga ggtctcagct gctctttc 900  
tgtatagccc cacagcagtc ttccccagca ccccaccaga ggagccagag 950  
gtgattcctc aagttagcct tgtgccacg ctggccctgc tgctggcct 1000  
gcccatccca tttgggata tcgggaaagt gatggctgag ctattctcag 1050  
ggggtgagga ctcccagccc cactcctctg cttagccca agcctcagct 1100  
ctccatctca atgctcagca ggtgtcccga tttcttcata cctactcago 1150  
tgctactcag gaccttcaag ctaaggagct tcattcagctg cagaacctct 1200  
tctccaaggc ctctgctgac taccagtggc ttctccagag ccccaagggg 1250  
gctgaggcga cactgccgac tgtgattgct gagctgcagc agttcctgcg 1300  
gggagctcg 9 gccatgtgca tcgagtcttgc ggctcggttc tctctggtcc 1350  
gcatggcggg gggtaactgct ctcttggctg cttcctgctt tatctgcctg 1400  
ctggcatctc agtggcaat atccccaggc tttccattct gccctctact 1450  
cctgacacct gtggcctgg gcctgggtgg gcccatacg 9 t atgctggac 1500  
tcctggAAC tattgagctg aagctagatc tagtgcttct aggggctgtg 1550  
gctgcagtga gtcatttcct ccctttctg tggaaaggct gggctggctg 1600  
ggggtccaag aggccccctgg caaccctgtt tcccatccct gggcccggtcc 1650  
tgttactcct gctgtttcgc ttggctgtgt tcttctctga tagttttgtt 1700  
gtagctgagg ccagggccac ccccttcattt ttgggctcat tcattcctgct 1750  
cctgggtgtc cagcttcaact gggagggcca gctgcttcca cctaagctac 1800  
tcacaatgcc ccgccttggc acttcagcca caacaaaccc cccacggcac 1850  
aatggtgcat atgcccgtgag gcttggattt gggttgttt tatgtacaag 1900  
gctagctggg cttttcattc gttgccctga agagacacct gtttgccact 1950

cctctccctg gctgagtcct ctggcatcca tggtggtgg tcgagccaag 2000  
aatttatggt atggagcttgc tgtggcggcg ctggtgccc tgttagctgc 2050  
cgtgcgttg tggcttcgcc gctatggtaa tctcaagagc cccgagccac 2100  
ccatgcttt tggcgctgg ggactgcccc taatggcatt gggtaactgct 2150  
gcctactggg cattggcgtc gggggcagat gaggctcccc cccgtatccg 2200  
ggtcctggtc tctggggcat ccatggtgct gcctcgggct gtagcaggc 2250  
tggctgcttc agggctcgcg ctgctgctt ggaaggctgt gacagtgctg 2300  
gtgaaggctg gggcaggcgc tccaaggacc aggactgtcc tcactccctt 2350  
ctcaggcccc cccacttctc aagctgactt ggattatgtg gtccctcaaa 2400  
tctaccgaca catgcaggag gagttccggg gccgggttaga gaggaccaaa 2450  
tctcagggtc ccctgactgt ggctgcttat cagttgggta gtgtctactc 2500  
agctgctatg gtcacagccc tcaccctgtt ggccttccca cttctgctgt 2550  
tgcatgcgga ggcgcatacgtc cttgtgttcc tgcttctgtt tctgcagagc 2600  
ttccttctcc tacatctgct tgctgctggg ataccctgtca ccacccctgg 2650  
tcctttact gtgccatggc aggcaacttc ggcttgggcc ctcatggcca 2700  
cacagacctt ctactccaca ggccaccaggc ctgtcttcc agccatccat 2750  
tggcatgcag cttcgtggg attcccagag ggtcatggct cctgtacttg 2800  
gctgcctgct ttgcttagtgg gagccaacac cttgcctcc cacctcctct 2850  
ttgcagtagg ttgcccactg ctccctgctt ggccttccct gtgtgagagt 2900  
caagggtgc ggaagagaca gcagccccca ggaaatgaag ctgatgccag 2950  
agtcagaccc gaggaggaag aggagccact gatggagatg cggctccggg 3000  
atgcgcctca gcacttctat gcagcaactgc tgcaagctggg cctcaagtac 3050  
ctctttatcc ttggatttca gattctggcc tggccttgg cagcctccat 3100  
ccttcgcagg catctcatgg tctggaaagt gttgccttct aagttcatat 3150  
ttgaggctgt gggcttcatt gtgagcagcg tggacttct cctgggcata 3200  
gctttggta tgagagtgga tggtgctgtg agctcctggc tcaggcagct 3250  
atttctggcc cagcagaggt agccttagtct gtgattactg gcacttggct 3300  
acagagagtg ctggagaaca gtgttagcctg gcctgtacag gtactggatg 3350  
atctgcaaga caggctcagc catactctta ctatcatgca gccaggggcc 3400

gctgacatct aggacttcat tattctataa ttcaggacca cagtggagta 3450  
tgatccctaa ctccctgattt ggatgcattt gagggacaag gggggcggtc 3500  
tccgaagtgg aataaaatag gccgggcgtg gtgacttgca cctataatcc 3550  
cagcactttg ggaggcagag gtgggaggat tgcttggtcc caggagttca 3600  
agaccagcct gtggaacata acaagacccc gtctctacta tttaaaaaaa 3650  
agtgtataaa aatgataata t 3671

<210> 102  
<211> 1089  
<212> PRT  
<213> Homo sapiens

<400> 102  
Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe  
1 5 10 15  
Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu  
20 25 30  
Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro  
35 40 45  
Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala  
50 55 60  
Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile  
65 70 75  
Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val  
80 85 90  
Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser  
95 100 105  
Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu  
110 115 120  
Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu  
125 130 135  
Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly  
140 145 150  
Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys  
155 160 165  
Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp  
170 175 180  
Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe  
185 190 195  
Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

200	205	210
Ile Leu Glu His Leu Tyr Pro Thr Met Asp Ser Gly Glu Trp Asp		
215	220	225
Val Leu Ile Ala His Phe Leu Gly Val Asp His Cys Gly His Lys		
230	235	240
His Gly Pro His His Pro Glu Met Ala Lys Lys Leu Ser Gln Met		
245	250	255
Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr		
260	265	270
Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp		
275	280	285
His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu		
290	295	300
Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro		
305	310	315
Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu		
320	325	330
Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala		
335	340	345
Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala		
350	355	360
Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser		
365	370	375
Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala		
380	385	390
Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala		
395	400	405
Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr		
410	415	420
Leu Pro Thr Val Ile Ala Glu Leu Gln Gln Phe Leu Arg Gly Ala		
425	430	435
Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg		
440	445	450
Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys		
455	460	465
Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys		
470	475	480
Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile		
485	490	495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu  
                   500                     505                     510  
 Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe  
                   515                     520                     525  
 Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala  
                   530                     535                     540  
 Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Phe  
                   545                     550                     555  
 Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala  
                   560                     565                     570  
 Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val  
                   575                     580                     585  
 Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu  
                   590                     595                     600  
 Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg  
                   605                     610                     615  
 His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu  
                   620                     625                     630  
 Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr  
                   635                     640                     645  
 Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met  
                   650                     655                     660  
 Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala  
                   665                     670                     675  
 Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg  
                   680                     685                     690  
 Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg  
                   695                     700                     705  
 Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala  
                   710                     715                     720  
 Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu  
                   725                     730                     735  
 Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu  
                   740                     745                     750  
 Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val  
                   755                     760                     765  
 Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu  
                   770                     775                     780  
 Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr

785	790	795
Val Val Pro Gln Ile Tyr Arg His Met Gln	Glu Glu Phe Arg Gly	
800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro	Leu Thr Val Ala Ala	
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala	Met Val Thr Ala Leu	
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	
845	850	855
Ser Leu Val Phe Leu Leu Phe Leu Gln	Ser Phe Leu Leu Leu	
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val Thr	Thr Pro Gly Pro Phe	
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala Trp	Ala Leu Met Ala Thr	
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln Pro	Val Phe Pro Ala Ile	
905	910	915
His Trp His Ala Ala Phe Val Gly Phe Pro	Glu Gly His Gly Ser	
920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val Gly	Ala Asn Thr Phe Ala	
935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys Pro	Leu Leu Leu Leu Trp	
950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg	Lys Arg Gln Gln Pro	
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val Arg	Pro Glu Glu Glu Glu	
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg Asp	Ala Pro Gln His Phe	
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys	Tyr Leu Phe Ile Leu	
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala	Ala Ser Ile Leu Arg	
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe Ala	Pro Lys Phe Ile Phe	
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser Val	Gly Leu Leu Leu Gly	
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly Ala Val	Ser Ser Trp Phe	
1070	1075	1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg  
1085

<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

tgccgctgcc gccgctgctg ctgttgcctc tggcgccgcac ttggggacgg 50  
gcagttccct gtgtctctgg tggttgcct aaacctgcaa acatcacctt 100  
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150  
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaattgg 200  
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250  
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgttcc 300  
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tggtaatac 350  
taaatcaaacc agaacgtggt cccagtgtgt gaccaaccac acgctggtc 400  
tcacccctggct ggagccgaac actcttact gcgtacacgt ggagtccctc 450  
gtccccaggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500  
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atttctgg 550  
atgttttgcctt catatcttatt accgtgttcc tttttctgt gatggctat 600  
tccatctacc gatataatcca cgtggccaa gagaaacacc cagcaaattt 650  
gattttgatt tatggaaatg aatttgacaa aagattctt gtgcctgctg 700  
aaaaaaatcgat gattaacttt atcaccctca atatctcgga tgattctaaa 750  
atttctcatc aggatatgag tttactggaa aaaagcagtg atgtatccag 800  
ccttaatgtat cctcagccca gcggaaacct gaggccccct caggaggaag 850  
aggaggtgaa acattttaggg tatgcttcgc atttgatggaa aattttttgt 900  
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtccct 950  
cagoagaaca ataccccccgg ataaaacagt cattgaatat gaatatgtat 1000  
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagttt 1050  
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcgtt 1100  
ggcagtcctg ggcccgaaaa cgttacagta ctcatacacc cctcagctcc 1150  
aagacttaga cccccctggcg caggagcaca cagactcgga ggagggcccg 1200  
gaggaagagc catcgacgac cctggtcgac tggatcccc aaactggcag 1250

gctgtgtatt ctttcgttgt ccagcttcga ccaggattca gagggtcg 1300  
agccttctga gggggatggg ctccggagagg agggtcttct atcttagactc 1350  
tatgaggagc cggtccaga caggccacca ggagaaaatg aaacctatct 1400  
catgcaattc atggaggaat ggggttata tgtgcagatg gaaaactgat 1450  
gccaacactt cctttgcct tttgttcct gtgcaaaca gtgagtcacc 1500  
ccttgatcc cagccataaa gtacctggga tgaaagaagt ttttccagt 1550  
ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600  
cgtgtgtat tggttcatgc atgttaggtct cttaacaatg atggtgggcc 1650  
tctggagtcc aggggctggc cggttgcct atgcagagaa agcagtcaat 1700  
aaatgtttgc cagactgggt gcagaattta ttcaagggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
1				5					10				15	

Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25				30	

Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
					35				40				45	

Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50				55				60		

Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70				75	

Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80				85				90		

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
					95				100				105	

His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110				115				120		

Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130				135	

Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140				145				150		

Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160			165		

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile
				170					175					180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys
				185					190					195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys
				200					205					210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val
				215					220					225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro
				230					235					240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu
				245					250					255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser
				260					265					270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys
				275					280					285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys
				290					295					300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser
				305					310					315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu
				320					325					330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp
				335					340					345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro
				350					355					360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr
				365					370					375
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser
				380					385					390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Gly	
				395					400					405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro
				410					415					420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly
				425					430					435
Leu	Tyr	Val	Gln	Met	Glu	Asn								
				440										

<210> 105

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct

<400> 105  
cgctgctgct gttgctcctg g 21

<210> 106  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 106  
cagtggtgcggc ggactttg 18

<210> 107  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 107  
agtccgcaggc agcggtgg 18

<210> 108  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 108  
ctcctccgag tctgtgtgct cctgc 25

<210> 109  
<211> 51  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence

<222> 1-51  
<223> Synthetic construct.

<400> 109  
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacat 50  
c 51

<210> 110  
<211> 1114  
<212> DNA  
<213> Homo sapiens

<400> 110  
cgacgcgtg ggcggacgcg tggcggacg cgtgggtctc tgccgggaga 50  
cgccagcctg cgtctgccat gggctcggg ttgaggggct gggacgtcc 100  
tctgctgact gtggccaccg ccctgatgct gcccgtgaag ccccccgag 150  
gctcctgggg ggcccagatc atcgggggcc acgaggtgac ccccccactcc 200  
aggccctaca tggcatccgt gcgcattcggg gccaaacatc actgcggagg 250  
cttcctgctg cgagcccgct gggtggtctc ggccgcccac tgcttcagcc 300  
acagagacct ccgcactggc ctggtggtgc tggcgccca cgtcctgagt 350  
actgcggagc ccacccagca ggtgtttggc atcgatgctc tcaccacgca 400  
ccccgactac caccccatga cccacgcca cgcacatctgc ctgctgcggc 450  
tgaacggctc tgctgtcctg gcgcattcggg tggggctgct gaggctgcca 500  
gggagaaggg ccaggccccc cacagcgggg acacggtgcc gggtggtgg 550  
ctggggcttc gtgtctgact ttgaggagct gcccgcggc ctgatggagg 600  
ccaagggtccg agtgctggac ccggacgtct gcaacagctc ctggaaggc 650  
cacctgacac ttaccatgct ctgcacccgc agtggggaca gccacagacg 700  
gggcttctgc tcggccgact ccggagggcc cctggtggtgc aggaaccggg 750  
ctcacggcct cgtttccctc tcgggcctct ggtgcggcga ccccaagacc 800  
cccgacgtgt acacgcaggt gtccgcctt gtggcctggc tctggacgt 850  
ggttcggcgg agcagtcccc agcccgcccc cctgcctggg accaccaggc 900  
ccccaggaga agccgcctga gccacaacct tgccgcattc aaatgagatg 950  
gccgctccag gcctggaaatg ttccgtggct gggccccacg ggaaggctga 1000  
tgttcagggt tgggggtggga cggcagcgg tggggcacac ccattccaca 1050  
tgcaaaggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111  
<211> 283  
<212> PRT  
<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
1				5					10					15
Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20				25						30
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
					35				40					45
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50				55						60
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65				70						75
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80				85						90
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95				100						105
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110				115						120
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125				130						135
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140				145						150
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155				160						165
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170				175						180
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185				190						195
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200				205						210
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215				220						225
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230				235						240
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245				250						255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly  
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala  
275 280

<210> 112  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 112  
gacgtctgca acagtcctcg gaag 24

<210> 113  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 113  
cgagaaggaa acgaggccgt gag 23

<210> 114  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 114  
tgacacttac catgctctgc acccgcaagt gggacagcca caga 44

<210> 115  
<211> 1808  
<212> DNA  
<213> Homo sapiens

<400> 115  
gagctaccca ggcggctgggt gtgcagcaag ctccgcgcgg actccggacg 50  
cctgacgcct gacgcctgtc cccggcccg catgagccgc tacctgctgc 100  
cgctgtcgcc gctgggcacg gtagcaggcg ccggcgtgct gctcaaggac 150  
tatgtcaccg gtggggcttg ccccagcaag gccaccatcc ctggaaagac 200

ggtcatcgta acgggcgcca acacaggcat cgggaagcag accgccttgg 250  
aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300  
aagtgtgagg cgccagcaaa ggacatccgc ggggagaccc tcaatcacca 350  
tgtcaacgcc cgccacctgg acttggcttc cctcaagtct atccgagagt 400  
ttgcagcaaa gatcattgaa gaggaggagc gagtgacat tctaataaac 450  
aacgcgggtg tgcgtcggtg cccccactgg accaccgagg acggcttcga 500  
gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550  
tgctggacaa gctgaaagcc tcagcccctt cgcggatcat caacctctcg 600  
tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650  
gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700  
tcgtcccttt caccaaggag ctgagccggc ggctgcaagg ctctgggttg 750  
actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tggcagaca 800  
cacgggcattc catggctcca ctttctccag caccacactc gggccatct 850  
tctggctgct ggtcaagagc cccgagctgg cgcggcagcc cagcacatac 900  
ctggccgtgg cggaggaact ggccgatgtt tccggaaagt acttcgatgg 950  
actcaaacag aaggccccgg ccccgaggc tgaggatgag gaggtggccc 1000  
ggaggctttg ggctgaaagt gcccgcctgg tggccttaga ggctccctct 1050  
gtgagggagc agccccctccc cagataacct ctggagcaga tttgaaagcc 1100  
aggatggcgc ctccagaccc aggacagctg tccgcctatgc ccgcagcttc 1150  
ctggcactac ctgagccggg agacccagga ctggcggccg ccatgcccgc 1200  
agttagttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250  
gcactgcccc gggctctggc tggccctggc tgctctgctg ccagcagggg 1300  
agagggggcca tctgatgctt cccctggaa tctaaactgg gaatggccga 1350  
ggaggaaggg gctctgtgca cttgcaggcc acgtcaggag agccagcggt 1400  
gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450  
tctgacactt ggtggattct tgggtccctg tgggaccttg tgcacatgc 1500  
gtcctctctg agccttgggtt tcttcagcag tggatgctc agaataactg 1550  
ctgtctccca tgcgtgtgtg gtacagcgag ctgttgcctg gctatggcat 1600  
ggctgtcggg ggggtgttttgcgtggcctt cctgtgccag agccagccca 1650

gagagcaggt gcaggtgtca tcccgagtgc aggctctgca cggcatggag 1700  
tggaaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750  
cacccctcta tcaattctca tggttagtcca aactgcagac tctcaaactt 1800  
gctcattt 1808

<210> 116  
<211> 331  
<212> PRT  
<213> Homo sapiens

<400> 116  
Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala  
1 5 10 15  
Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys  
20 25 30  
Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
35 40 45  
Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
50 55 60  
Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
65 70 75  
Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
80 85 90  
Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
95 100 105  
Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
110 115 120  
Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
125 130 135  
Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
140 145 150  
Phe Leu Leu Thr Asn Leu Leu Asp Lys Leu Lys Ala Ser Ala  
155 160 165  
Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
170 175 180  
His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn  
185 190 195  
Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe  
200 205 210  
Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val  
215 220 225

Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His  
230 235 240

Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro  
245 250 255

Ile Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro  
260 265 270

Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly  
275 280 285

Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala  
290 295 300

Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg  
305 310 315

Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln Pro Leu Pro  
320 325 330

Arg

<210> 117  
<211> 2249  
<212> DNA  
<213> Homo sapiens

<400> 117  
gaagttcgcg agcgctggca tgtggtcctg gggcgccgct ggccgcgcgt 50  
ctggcggtgc tggcgctcgg gacaggagac ccagaaaagg ctgcggctcg 100  
gggcgacacg ttctcggcgc tgaccagcgt ggccgcgcgc ctggcgcccc 150  
agcgccggct gctggggctg ctgaggcggt acctgcgcgg ggaggaggcg 200  
cggctgcggg acctgacttag attctacgac aaggtacttt ctttgcattga 250  
ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300  
aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
gagaacatcc gagctctgaa ggtggctat gagaagggtgg agcaagacct 400  
tccagccttt gaggaccttg agggagcagc aaggccctg atgcggctgc 450  
aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtcttcag 500  
agagtcaactg gctctgccat cactgacctg tacagcccc aacggctctt 550  
ttctctcaca gggatgact gctccaagt tggcaagggtg gcctatgaca 600  
tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650  
ttccgaggat cttacggaga gtgaaagaca gaggatgagg caagtctaga 700

agatgcctg gatcaacttgg cctttgctta tttccggca ggaaatgtt 750  
cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800  
aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
ccccaaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900  
acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950  
cagcccactc tctaccagat ccctagcctc tactgttccct atgagaccaa 1000  
ttccaaacgccc tacctgctgc tccagccat ccggaaggag gtcatccacc 1050  
tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100  
cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtggtgcc 1150  
atcaggggag aagcagttac aagtggagta ccgcattcagc aaaagtgcct 1200  
ggctgaagga cactgttgc acaaaactgg tgaccctcaa ccaccgcatt 1250  
gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300  
ggtgtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350  
ctacgtcacc aagcagcccc ctctacagaa tgaagtcaagg aaaccgagtt 1400  
gcaacattta tgatctatct gagctcggtg gaagctggag gagccacagc 1450  
cttcatctat gccaacctca gcgtgcctgt ggttaggaat gcagcactgt 1500  
tttggtggaa cctgcacagg agtggtgaag gggacagtga cacacttcat 1550  
gctggctgtc ctgtccttgtt gggagataag tgggtggcca acaagtggat 1600  
acatgagttt ggcacaggaat tccgcagacc ctgcagctcc agccctgaag 1650  
actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700  
aagccaggag ccaaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750  
ctggagaag gccttgcag cttgtctgt gcctcgcaaa tcagaggcaa 1800  
gggagagggtt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850  
agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtgga 1900  
ggcctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950  
acatctcaac agtctcaggt tcgatcagtg ggtctttgg cactttgaac 2000  
cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050  
tagcctgact cccagaacct taagactttc tccccactgc cttctgctgc 2100  
agcccaagca gggagtgcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala
1				5					10				15	

Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr
				20					25				30	

Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg
					35				40				45	

Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala
				50					55				60	

Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu
				65					70				75	

His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe
				80					85				90	

Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His
				95					100				105	

Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr
				110					115				120	

Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly
				125					130				135	

Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn
				140					145				150	

Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser
				155					160				165	

Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr
				170					175				180	

Gly	Asp	Asp	Cys	Phe	Gln	Val	Gly	Lys	Val	Ala	Tyr	Asp	Met	Gly
				185					190				195	

Asp	Tyr	Tyr	His	Ala	Ile	Pro	Trp	Leu	Glu	Glu	Ala	Val	Ser	Leu
				200					205				210	

Phe	Arg	Gly	Ser	Tyr	Gly	Glu	Trp	Lys	Thr	Glu	Asp	Glu	Ala	Ser
				215					220				225	

Leu	Glu	Asp	Ala	Leu	Asp	His	Leu	Ala	Phe	Ala	Tyr	Phe	Arg	Ala
				230					235				240	

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu  
                   245                  250                  255  
 Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr  
                   260                  265                  270  
 Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala  
                   275                  280                  285  
 Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr  
                   290                  295                  300  
 Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr  
                   305                  310                  315  
 Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala  
                   320                  325                  330  
 Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu  
                   335                  340                  345  
 Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala  
                   350                  355                  360  
 Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val  
                   365                  370                  375  
 Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser  
                   380                  385                  390  
 Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr  
                   395                  400                  405  
 Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro  
                   410                  415                  420  
 Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly  
                   425                  430                  435  
 His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro  
                   440                  445                  450  
 Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile  
                   455                  460                  465  
 Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr  
                   470                  475                  480  
 Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp  
                   485                  490                  495  
 Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His  
                   500                  505                  510  
 Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys  
                   515                  520                  525  
 Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser

530

535

540

Ser Pro Glu Asp

<210> 119  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 119  
cgggacagga gacccagaaa ggg 23

<210> 120  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 120  
ggccaagtga tccaaaggcat cttc 24

<210> 121  
<211> 49  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-49  
<223> Synthetic construct.

<400> 121  
ctgcgggacc tgacttagatt ctacgacaag gtactttctt tgcatgggg 49

<210> 122  
<211> 1778  
<212> DNA  
<213> Homo sapiens

<400> 122  
gagataggga gtctgggtt aagttcctgc tccatctcag gagcccctgc 50  
tccccccctt aggaagccac cagactccac ggtgtggggc caatcaggtg 100  
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150  
ggagagcccc ggagcccccg taacccgcgc ggggagcgcc caggatgccg 200

cgcgccccact cgagcagggt gcgctactgc gcgcgttct cctacctctg 250  
gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300  
ccctggtcct gtctgtggc atctatgcag aggttgcgcg gcagaaatat 350  
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatacctcct 400  
gggcgtcgtc atgttcatgg ttccttcattt tggtgtgctg gcgtccctcc 450  
gtgacaacctt gtaccttctc caagcattca tgtacatcct tggatctgc 500  
ctcatcatgg agctcatgg tggcgtggtg gccttgacct tccggAACCA 550  
gaccattgac ttccctgaacg acaacattcg aagaggaatt gagaactact 600  
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650  
aagtgcgttg gcggggagga ctaccgagat tggagcaaga atcagtagcca 700  
cgactgcagt gcccctggac ccctggcctg tgggtgccc tacacctgct 750  
gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800  
atcgacaagg agcgtttcag tgtgcaggat gtcatacgt tgccgggctg 850  
caccaacgcc gtgatcatct ggttcatggca caactacacc atcatggcgt 900  
gcatccctcct gggcatcctg cttcccccagt tcctgggggt gctgctgacg 950  
ctgctgtaca tcacccgggt ggaggacatc atcatggagc actctgtcac 1000  
tgcgtggctc ctggggcccg gtgcacggcc cagcgtggag gcggcaggca 1050  
cgggatgctg cttgtgctac cccaattagg gcccagcctg ccatggcagc 1100  
tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150  
ggacagggt gcggccctc tgcccacact cagtaactgac caaagccagg 1200  
gctgtgttg cctgtgtgtt ggtccacgg cctctgcctc cccagggagc 1250  
agagcctggg cttccctaa gaggcttcc ccgaggcagc tctggaatct 1300  
gtgcccacct gggccctggg gaacaaggcc ctccttctc caggcctggg 1350  
ctacagggga gggagagcct gaggctctgc tcagggccca tttcatctct 1400  
ggcagtgcct tggcggttgtt attcaaggca gttttgttagc acctgttaatt 1450  
ggggagaggg agtgtgcctt tcggggcagg agggaaaggc atctggggaa 1500  
gggcaggagg gaagagctgt ccatgcagcc acgcccattgg ccaggttggc 1550  
ctcttctcag cttccctagggt gccttgagcc ctcttgcaag ggcggctgct 1600  
tccttgagcc tagttttttt ttacgtgatt tttgttaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttcccccgc 1700  
gtcttattct tgcccttccc ccaaccagtt tgttaatcaa acaataaaaa 1750  
catgtttgt tttgtttta aaaaaaaaa 1778

<210> 123  
<211> 294  
<212> PRT  
<213> Homo sapiens

<400> 123  
Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe  
1 5 10 15  
Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val  
20 25 30  
Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala  
35 40 45  
Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu  
50 55 60  
Ala Pro Ala Ile Ile Leu Ile Leu Gly Val Val Met Phe Met  
65 70 75  
Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr  
80 85 90  
Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met  
95 100 105  
Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr  
110 115 120  
Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr  
125 130 135  
Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys  
140 145 150  
Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys  
155 160 165  
Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly  
170 175 180  
Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn  
185 190 195  
Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val  
200 205 210  
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile  
215 220 225  
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly



<400> 127  
gaggagcggg ccgaggactc cagcgtgcc aggtctggca tcctgcactt 50  
gctgccctct gacacctggg aagatggccg gcccgtggac cttcaccctt 100  
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtcccac 150  
tgcagttctc atcctcgcc caaaagtcat caaagaaaag ctgacacagg 200  
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250  
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tggcagcct 300  
ggtaaacacc gtcctgaagc acatcatctg gctgaaggc atcacagcta 350  
acatcctcca gctgcaggtg aagccctcg ccaatgacca ggagctgcta 400  
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtaa 450  
gaccatcgta gagttccaca tgacgactga ggcccaagcc accatccgca 500  
tggacaccag tgcaagtggc cccacccgcc tggcctcag tgactgtgcc 550  
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttcct 600  
ggtaaacgcc tttagctaagc aggtcatgaa ctccttagtg ccatccctgc 650  
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccattcaat 700  
ggcatgtatg cagacctcct gcagctggtg aaggtgcca tttccctcag 750  
cattgaccgt ctggagtttgc accttctgtt tcctgccatc aagggtgaca 800  
ccattcagct ctacctgggg gccaagttgt tggactcaca gggaaagggtg 850  
accaagtggc tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900  
caacatcccg tttagcctca tcgtgagtcg ggacgtggtg aaagctgcag 950  
tggctgctgt gctctctcca gaagaattca tggcctgtt ggactctgtg 1000  
cttcctgaga gtgcccatcg gctgaagtca agcatcgccg tgatcaatga 1050  
aaaggctgca gataagctgg gatctaccca gatcgtgaag atcctaactc 1100  
aggacactcc cgagttttt atagaccaag gccatgcca ggtggccaa 1150  
ctgatcgtgc tggaaagtgtt tccctccagt gaagccctcc gccctttgtt 1200  
caccctgggc atcgaagcc gctcggaaagc tcagtttac accaaagggtg 1250  
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300  
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350  
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400  
gatctgggggt cccagtgtca ttggtaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttgtc cttactccag ctccttgtc 1500  
gaaaccgc ttcctgtct cccagtgaag acttggatgg cagccatcg 1550  
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600  
cctcttgca atcaataaac acttgctgt gaaaaa 1636

<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
1				5				10						15
Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
			20				25							30
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
			35				40							45
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
				50				55						60
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
			65				70							75
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
			80				85							90
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
			95				100							105
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
			110				115							120
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
			125				130							135
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
			140				145							150
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
			155				160							165
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu
			170				175							180
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu
			185				190							195
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly
			200				205							210
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu
			215				220							225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys  
                  230                     235                     240  
 Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser  
                  245                     250                     255  
 Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu  
                  260                     265                     270  
 Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser  
                  275                     280                     285  
 Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu  
                  290                     295                     300  
 Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His  
                  305                     310                     315  
 Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp  
                  320                     325                     330  
 Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr  
                  335                     340                     345  
 Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu  
                  350                     355                     360  
 Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu  
                  365                     370                     375  
 Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr  
                  380                     385                     390  
 Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp  
                  395                     400                     405  
 Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp  
                  410                     415                     420  
 Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu  
                  425                     430                     435  
 Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu  
                  440                     445                     450  
 Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys  
                  455                     460                     465  
 Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser  
                  470                     475                     480  
 Pro Val Ser Gln

<210> 129  
 <211> 2213  
 <212> DNA  
 <213> Homo sapiens

<400> 129  
gagcgaacat ggcagcgct tggcggttt ggtgtgtctc tgtgaccatg 50  
gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccccaaag 100  
aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atgaaatgga 150  
ctaacaaaag acctgtataa agaatgaatg gagacaagtt ccgtcgccctt 200  
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcactgctct 250  
ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300  
agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350  
tttttgcca tggtgattt tgatgaaggc tctgatgtat ttcagatgct 400  
aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaaggaaac 450  
ccaaacgggg tgatacatat gagttacagg tgcggggttt ttcagctgag 500  
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550  
tagaccccca aattatgctg gtcccccattt gttgggattt cttttggctg 600  
ttattggtg acttgtgtat cttcgaagaa gtaatatgga atttctctt 650  
aataaaaactg gatgggctt tgcagctttg tgttttgtgc ttgctatgac 700  
atctggtcaa atgtgaaacc atataagagg accaccat gcccataaga 750  
atccccacac gggacatgtg aattatatcc atggaaacag tcaagcccag 800  
ttttagctg aaacacacat tgttctctg ttaatggtg gagttacatt 850  
aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900  
agcgaaagat aatgtgtgtg gctggtaattg gacttgtgtt attattctc 950  
agttggatgc tctctatttt tagatctaaa tatcatggct acccatacag 1000  
ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtaact 1050  
ggaaattgaa aaacgaaaat cgtgtgttt tgaaaagaag aatgcaactt 1100  
gtatattttg tattacctct tttttcaag tgatttaat agttaatcat 1150  
ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaat 1200  
ctgaggtatt tgaaaataat tatcctctta accttcttcccaggtaac 1250  
tttatggAAC atttaattta gtacaattaa gtatattata aaaattgtaa 1300  
aactactact ttgttttagt tagaacaaag ctcaaaaacta ctttagttaa 1350  
cttggtcattc tgattttata ttgccttata caaagatggg gaaagtaagt 1400  
cctgaccagg tgttccacaca tatgcctgtt acagataact acattaggaa 1450

ttcattctta gcttcttcat ctttgtgtgg atgtgtatac tttacgcata 1500  
tttcctttg agtagagaaa ttatgtgtgt catgtggct tctgaaaatg 1550  
gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600  
ctcctccctcc ttgcataattt cctactgcgc tccagcctga gtgatagagt 1650  
gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataattct 1700  
gcttgagttat ggtgttaact accttgcatt tagaaagatt tcagattcat 1750  
tccatctcct tagtttctt ttaaggtgac ccatctgtga taaaaatata 1800  
gcttagtgct aaaatcagtg taacttatac atggcctaaa atgtttctac 1850  
aaatttagagt ttgtcactta ttccatttgc acctaagaga aaaataggct 1900  
cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950  
tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000  
gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050  
attagctggg tgtggtggca ggaggctgta atcccagcta cacaggaggc 2100  
tgaggcacga gaatcacttg aactcaggag atggagggtt cagtggccg 2150  
agatcacgcc actgcactcc agcctggcaa cagagcggaa ctccatctca 2200  
aaaaaaaaaa aaa 2213

<210> 130  
<211> 335  
<212> PRT  
<213> Homo sapiens

<400> 130  
Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val  
1 5 10 15  
Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln  
20 25 30  
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met  
35 40 45  
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys  
50 55 60  
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile  
65 70 75  
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys  
80 85 90  
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg  
95 100 105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp
								110				115		120
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser
								125				130		135
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg
								140				145		150
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln
								155				160		165
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val
								170				175		180
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu
								185				190		195
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met
								200				205		210
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys
								215				220		225
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg
								230				235		240
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn
								245				250		255
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His
								260				265		270
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu
								275				280		285
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys
								290				295		300
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser
								305				310		315
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr
								320				325		330
Ser	Phe	Leu	Met	Ser										
				335										

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

aagcaaccaa actgcaagct ttgggagttt ttcgctgtcc ctgccctgct 50

ctgctaggga gagaacgcca gagggaggcg gctggcccg 100

tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150  
cttggcgctg gcggtaactgg ccccccggagc aggggagcag aggcggagag 200  
cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc ctgcgtatgga 250  
aggtaacat ttcatccagg aagttaggtt gtgaaacttc cttttatcaa 300  
cttttatgaag acacgtggga cttccttctt gaatgcctac acaaactctc 350  
caatttggtg cccatcacgc gcagcaatgt ggagtggctt cttcactcac 400  
ttaacagaat ctggaaataa ttttaagggtt ctagatccaa attataacaac 450  
atggatggat gtcatggaga ggcattggcta ccgaacacag aaatttggga 500  
aactggacta tacttcagga catcactcca ttagtaatcg tgtggaaagcg 550  
tggacaagag atgttgctt cttactcaga caagaaggca ggcccatgg 600  
taatcttatac cgtaacagga ctaaagttagt agtgatggaa aggattggc 650  
agaatacaga caaagcagta aactggtaa gaaaggaagc aattaattac 700  
actgaaccat ttgttattta cttgggattta aatttaccac acccttaccc 750  
ttcaccatct tctggagaaa atttggatc ttcaacattt cacacatctc 800  
tttattggct tgaaaaagtgt tctcatgtt ccatcaaaat cccaaagtgg 850  
tcacccttgtt cagaaatgca ccctgttagat tattactt cttataaaaa 900  
aaactgcact ggaagattta caaaaaaaga aattaagaat attagagcat 950  
tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000  
ttggcccttc atcaattaga tcttcttcag aaaactattt tcatataactc 1050  
ctcagaccat ggagagctgg ccatggaca tcgacagttt tataaaatga 1100  
gcatgtacga ggcttagtgca catgttccgc tttttagatgat gggaccagga 1150  
attaaagccg gcctacaagt atcaaatgtg gtttcttgc tggatattta 1200  
ccctaccatg cttgatattt cttggattcc tctgcctcag aacctgagtg 1250  
gatactctt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300  
gtcaaaaacc tgcattccacc ctggattctg agtgaattcc atggatgtaa 1350  
tgtgaatgcc tccacccatac tgcttcgaac taaccactgg aaatatata 1400  
cctattcggta tggtgcatca atattgcctc aactcttgc tcttcctcg 1450  
gatccagatg aattaacaaa tggatgttgc aaatttccag aaattactta 1500  
ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600  
ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650  
ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700  
aaaccatat gaatccaaga gcagttgaa caaaaagttt aaaaatagtg 1750  
ttcttagagat acatataaat atattacaag atcataatta tgtatcaa 1800  
atgaaacagt tttataattt accaagttt ggccgggcac agtggctcac 1850  
acctgtaatc ccaggactt gggaggctga ggaaagcaga tcacaaggc 1900  
aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950  
aaatacaaaa attagctggg cgcggtggtg cacacctata gtctcagcta 2000  
ctcagaggct gaggcaggag gatcgctga acccgggagg cagcagttgc 2050  
agtgagctga gattgcgcca ctgtactcca gcctggcaac agagtgagac 2100  
tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aattttcat 2150  
tattttgtaa gaatgttagt tatttaaga taaaatgccatgattataa 2200  
aatcacatat tttcaaaaat gtttattt taggccttg tacaatttct 2250  
aacaatttag tggaagtatc aaaaggattt aagcaaatac tgtaacagtt 2300  
atgttccttt aaataataga gaatataaaa tattgtataataatgtatca 2350  
taaaaatagtt gtatgtgagc attttaggtt gaaaaaaaaaaaaaaaaa 2400  
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2450  
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaa 2476

<210> 132  
<211> 536  
<212> PRT  
<213> Homo sapiens

<400> 132  
Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala  
1 5 10 15  
Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys  
20 25 30  
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg  
35 40 45  
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile  
50 55 60  
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr  
65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly
				80					85				90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu
				95					100			105		
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly
				110					115			120		
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His
				125					130			135		
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala
				140					145			150		
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg
				155					160			165		
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr
				170					175			180		
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr
				185					190			195		
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr
				200					205			210		
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His
				215					220			225		
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys
				230					235			240		
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr
				245					250			255		
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys
				260					265			270		
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu
				275					280			285		
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu
				290					295			300		
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly
				305					310			315		
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr
				320					325			330		
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile
				335					340			345		
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile
				350					355			360		
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys 380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser 395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg 410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile 425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr 440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln 455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val 470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile 485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln 500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln 515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val 530	535	

<210> 133  
<211> 1475  
<212> DNA  
<213> Homo sapiens

<400> 133  
gagagaagtc agcctggcag agagactctg aaatgaggga ttagaggtgt 50  
tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100  
gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtgg 150  
ctacatccta ggccttctgg ggctttggg cacactggtt gccatgctgc 200  
tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250  
gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300  
catcacccag tgtgacatct atagcaccct tctggcctg cccgctgaca 350  
tccaggctgc ccaggccatg atggtgacat ccagtgaat ctccctccctg 400  
gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atcccgagcc aaagacagag tggcggtagc aggtggagtc ttttcatcc 500  
ttggaggcct cctgggattc attcctgttgc cctggaatct tcataggatc 550  
ctacgggact tctactcacc actggtgccc gacagcatga aattttagat 600  
tggagaggct cttaacttgg gcattatttc ttccctgttc tccctgatag 650  
ctggaatcat cctctgcttt tcctgctcat cccagagaaa tcgctccaac 700  
tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750  
gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800  
cagggtatgt gtgaagaacc aggggccaga gctgggggt ggctgggtct 850  
gtaaaaaaca gtggacagca ccccgaggc cacaggtgag ggacactacc 900  
actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950  
ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcagggtga 1000  
attgccaagg atgctcgcca tgccagcctt tctgtttcc tcaccttgct 1050  
gctccctgc cctaagtccc caaccctcaa cttgaaaccc cattccctta 1100  
agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150  
ccccaaaccc actaatcaca tcccaactgac tgaccctctg tgatcaaaga 1200  
ccctctctct ggctgagggtt ggctcttagc tcattgctgg ggatggaaag 1250  
gagaagcagt ggctttgtg ggcattgctc taacctactt ctcaagcttc 1300  
cctccaaaga aactgatgg ccctggaacc tccatccac tcttggat 1350  
actccacagt gtccagacta atttgtcat gaactgaaat aaaaccatcc 1400  
tacggtatcc agggAACAGA aagcaggatg caggatgggaa ggacaggaag 1450  
gcagcctggg acatttaaaa aaata 1475

<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu
1														15

Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
														30

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
														45

Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50	55	60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala		
65	70	75
Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile		
80	85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr		
95	100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala		
110	115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro		
125	130	135
Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro		
140	145	150
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr		
155	160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile		
170	175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr		
185	190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg		
200	205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser		
215	220	225
Leu Thr Gly Tyr Val		
230		

<210> 135

<211> 610

<212> DNA

<213> Homo sapiens

<400> 135

gcactgctgc tgtccatca gctgctctga agctccatgg tgcccagaat 50

cttcgctcct gtttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100

aagtcatcgc tcccgctggc tcagaaccat ggctgtgcc a cccggcaccc 150

aggtgtggag acaagatcta caaccccttg gagcagtgct gttacaatga 200

cgcacatcgtc tccctgagcg agacccgcc a tgggtccc ccctgcaccc 250

tctggccctg ctttgagctc tgctgtcttg attccttgg cctcacaaac 300

gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaaat gtgaaagcag aagacgttt ccctgagaag 400  
acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
atgacagtag attatcagga aataaataaa gtggttttc caatgtacac 600  
acctgtaaaa 610

<210> 136  
<211> 119  
<212> PRT  
<213> Homo sapiens

<400> 136  
Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu  
1 5 10 15  
Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu  
20 25 30  
Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
35 40 45  
Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
50 55 60  
Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys  
65 70 75  
Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe  
80 85 90  
Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser  
95 100 105  
Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro  
110 115

<210> 137  
<211> 771  
<212> DNA  
<213> Homo sapiens

<400> 137  
ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50  
gtcttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100  
agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150  
gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
gtcgtgccct tggccaggac ccagacgtgt ggaaactgca cttcagagt 250

ctgcttgag cagtgcgtcc cctggacatt catggtaag ctgataaacc 300  
agaactgcga ctcagcccg acctcgatg acaggcttg tcgcagtgtc 350  
agctaatttga acatcaggaa aacgatgact cctggattct cttcctggg 400  
tggccttggaa gaaagaggct ggtgttacct gagatctggg atgctgagt 450  
gctgtttgggg ggccagagaa acacacactc aactgcccac ttcatctgt 500  
gacctgtctg aggcccaccc tgcaagctgcc ctgaggaggc ccacaggtcc 550  
ccttcttagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600  
ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650  
accccaaggc tggctgggaa accttcacc cttctgtgag attttccatc 700  
atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750  
tatgtacttt ataaaatgaaa a 771

<210> 138  
<211> 110  
<212> PRT  
<213> Homo sapiens

<400> 138  
Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys 15  
1 5 10 15  
Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met 30  
20 25 30  
Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp 45  
35 40 45  
Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val 60  
50 55 60  
Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg 75  
65 70 75  
Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu 90  
80 85 90  
Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu 105  
95 100 105  
Cys Arg Ser Val Ser  
110

<210> 139  
<211> 2044  
<212> DNA  
<213> Homo sapiens

<400> 139

gggggcgggt gcctggagca cggcgctggg gccgcccga ggcgtcactc 50  
gctcgactc agtcgcggga ggctccccg cgccggccgc gtcccgccccg 100  
ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150  
cccacggccc tggaggccgg cagctggcgc tggggatccc tgctttcgc 200  
tctcttcctg gctgcgtccc taggtccggt ggcagccttc aaggtcgcca 250  
cgccgtattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300  
tgcaaggctct tggccctgt ggacaaaggg cacgatgtga ccttctacaa 350  
gacgtggtac cgcaagctoga gggcgaggt gcagacctgc tcagagcgcc 400  
ggcccatccg caacctcacg ttccaggacc ttcacctgca ccatggaggc 450  
caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500  
gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550  
ccctgctgga tagcggcctc tactgctgcc tggtggtgga gatcaggcac 600  
caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650  
aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctccagg 700  
atagtaaaaa catcacggct gcagccctgg ctacgggtgc ctgcacatgta 750  
ggaatcctct gcctccccc catcctgctc ctggtctaca agcaaaggca 800  
ggcagcctcc aaccggccgtg cccaggagct ggtgcggatg gacagcaaca 850  
ttcaaggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900  
atacccgagg ccaaagtca gCACCCCTG tcctatgtgg cccagcggca 950  
gccttctgag tctggcggc atctgcttc ggagcccagc acccccctgt 1000  
ctcctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 1050  
gactctccaa actttgaggt catctagccc agctggggga cagtggctg 1100  
ttgtggctgg gtctgggca ggtgcatttg agccaggct ggctctgtga 1150  
gtggcctccct tggcctcgcc cctggttccc tccctcctgc tctgggctca 1200  
gatactgtga catcccagaa gcccagcccc tcaacccttc tggatgctac 1250  
atggggatgc tggacggctc agccctgtt ccaaggattt tggggtgctg 1300  
agattctccc ctagagaccc taaattcacc agctacagat gccaatgac 1350  
ttacatctta agaagtctca gaacgtccag cccttcagca gctctcggtc 1400  
tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

tggccaccc tcccaggcac cagacacagg gcacggtgg a g a g a c t t c t c 1500  
ccccgtggcc gccttggctc ccccgtttg cccgaggctg ctcttctgtc 1550  
agacttcctc tttgtaccac agtggctctg gggccaggcc tgctgc cca 1600  
ctggccatcg ccacccccc cagctgcctc ctaccagcag tttctctgaa 1650  
gatctgtcaa caggtaagt caatctgggg cttccactgc ctgcattcca 1700  
gtccccagag ctgggtggc ccgaaacggg a a g t a c a t a t t g g g g c a t g g 1750  
tggcctccgt gagcaa atgg tgtcttggc a a t c t g a g g c c a g g a c a g a t 1800  
gttgccccac ccactggaga tggtgctgag ggagg tgggt gggccttct 1850  
gggaaggta gtggagagg gcacctgccc cccgcctcc ccatccccta 1900  
ctcccactgc tcagcgcggg ccattgcaag ggtgccacac a a t g t c t t g t 1950  
ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly
1														
														15

Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val
														30

Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro
														45

Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val
														60

Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser
														75

Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg
														90

Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln
														105

Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu
														120

Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn
														135

Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140	145	150
Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 cccacgcgtc cgccgccttc ctttctgtcg gacccctt cgtctctcca 50  
 tctcccttc ctccccgc gttcttttc cacctttctc ttctccac 100  
 cttagacctc cttcctgcc ctctttctt gcccaccgct gctcctggc 150  
 cttctccga ccccgctcta gcagcagacc tcctgggtc tgtgggtga 200  
 tctgtggccc ctgtgcctcc gtgtccttt cgtctccctt cttcccgact 250  
 ccgctccgg accagcggcc tgaccctgg gaaaggatgg ttcccgaggt 300  
 gagggtcctc tcctccttgc tggactcgc gctgctctgg ttccccctgg 350  
 actcccacgc tcgagccgc ccagacatgt tctgccttt ccatggaaag 400  
 agatactccc cggcgagag ctggcacccc tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500  
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550  
cagcaatgct gtcccaagtg tgtggAACCT cacactccct ctggactccg 600  
ggccccacca aagtccctgcc agcacaacgg gaccatgtac caacacggag 650  
agatcttcag tgcccattgag ctgttcccct cccgcctgcc caaccagtgt 700  
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750  
ccccgaacca ggctgcccag caccctccc actgccagac tcctgctgcc 800  
aaggcctgcaa agatgaggca agtgagcaat cgatgaaga ggacagtgtg 850  
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgtatgc 900  
tgggagaaaag agaggcccg gcaccccagc ccccaactggc ctcagcgccc 950  
ctctgagctt catccctcgc cacttcagac ccaagggagc aggtagcaca 1000  
actgtcaaga tcgtcctgaa ggagaaacat aagaaaggct gtgtgcattgg 1050  
cgggaaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100  
tcggccccctt gccctgcacat ctatgcacat gtgaggatgg cccggcaggac 1150  
tgccagcgtg tgacctgtcc caccgagttac ccctgccgtc accccgagaa 1200  
agtggctggg aagtgcgtca agatttgcac agaggacaaa gcagaccctg 1250  
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300  
ctcgccaca catcggtatc cccaaagccca gacaacctgc gtcgcttgc 1350  
cctggaacac gaggcctcgg acttgggtgga gatctacctc tggaaagctgg 1400  
taaaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450  
ccacacagcc agaatcttcc acttgactca gatcaagaaa gtcaggaagc 1500  
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggcccccac 1550  
gaaggtcact ggaacgtctt cctagcccaag accctggagc tgaaggtcac 1600  
ggccagtcac gacaaagtga ccaagacata acaaagacat aacagttgca 1650  
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700  
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142  
<211> 451  
<212> PRT  
<213> Homo sapiens

<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala
1				5				10					15	
Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp
				20				25					30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser
				35				40					45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg
				50				55					60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His
				65				70					75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln
				80				85					90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg
				95				100					105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His
				110				115					120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro
				125				130					135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys
				140				145					150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro
				155				160					165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu
				170				175					180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg
				185				190					195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly
				200				205					210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe
				215				220					225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val
				230				235					240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly
				245				250					255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg
				260				265					270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly
				275				280					285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
440	445	450
Thr		
<210> 143		
<211> 693		
<212> DNA		
<213> Homo sapiens		
<400> 143		
ctagcctgcg ccaagggtta gtgagaccgc gcggcaacag cttgcggctg 50		
cggggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100		
cttgcggaaa atgctgatct cagtgcata gctggcgca ggggctggcg 150		
tgggctacgc gtcctcggt atcgtgaccc cgggagagcg gcggaaagcag 200		
gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250		
ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgaacca 300		
cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350		
ggcgcaggcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgcgg 400		
gaccttggct tggcgcagg aatccgaggc agcctttctc cttcgtggc 450		

ccagcggaga gtccggaccc agataccatg ccaggactct ccggggtcct 500  
gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550  
tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
aactgaaaga accaataaaa tcatgttcct caaaaaaaaaaaaaaa 650  
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaa 693

<210> 144  
<211> 93  
<212> PRT  
<213> Homo sapiens

<400> 144  
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
1 5 10 15  
Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
20 25 30  
Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
35 40 45  
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
50 55 60  
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
65 70 75  
Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Ala Ser Gly  
80 85 90  
Arg Ser Pro

<210> 145  
<211> 1883  
<212> DNA  
<213> Homo sapiens

<400> 145  
caggagagaa ggcaccggcc ccaccccgcc tccaaagcta accctcgccc 50  
tttaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100  
caggctgcca tggggcccaag caccctctc ctcatcttgt tcctttgtc 150  
atggtcggga cccctccaag gacagcagca ccaccttgg gagtacatgg 200  
aacgcccact agctgctta gaggAACGGC tggcccagtg ccaggaccag 250  
atgatcgcc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
acaccatctc cgggagagtg gatcgctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagttgatg agaaggtgac 450  
tggaggccct gggaccaaag gcaagggaaag aaggaatgag aagtacgata 500  
tggtgacaga ctgtggctac acaatctctc aagttagatc aatgaagatt 550  
ctgaagcgat ttggtgccc agctggtcta tggaccaagg atccactggg 600  
gcaaacagag aagatctacg tgttagatgg gacacagaat gacacagcct 650  
ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccgaaa 700  
gcttccccgag tccgggtgcc cttccctgg gtaggcacag ggcagctgg 750  
atatggtggc tttctttatt ttgctcgag gcctcctgga agacctggtg 800  
gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850  
aaccgaacag tggtggacag ctcagtattc ccagcagagg ggctgatccc 900  
cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950  
aaggctttg ggctgttat gccacccggg aggatgacag gcacttgtt 1000  
ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050  
accatgtccc agagagaatg ctgaggctgc ctttgcatac tgtggaccc 1100  
tctatgtcgt ctataacacc cgtcctgcc a tgcggcccg catccagtgc 1150  
tcctttgatg ccagcggcac cctgacccct gaacggcag cactccctta 1200  
ttttccccgc agatatggtg cccatgccag cctccgttat aaccccccag 1250  
aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300  
gagatgagga agaaagagga ggaggttga ggagctagcc ttgtttttg 1350  
catcttctc actcccatac atttatatta tatccccact aaatttctt 1400  
ttcctcattc ttcaaattgtg ggccagttgt ggctcaaattc ctctatattt 1450  
ttagccaatg gcaatcaaatt tcttcagct ctttgcattc atacggaact 1500  
ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550  
ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600  
cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggg 1650  
agcagtgttc ttcccctcag agtgacttgg ggagggagaa ataggaggag 1700  
acgtccagct ctgtcctctc ttccctcactc ctcccttcag tgtcctgagg 1750  
aacaggactt tctccacatt gtttgcattt gcaacatttt gcattaaaag 1800  
aaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212>. PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp  
1 5 10 15

Ser Gly Pro Leu Gln Gln Gln His His Leu Val Glu Tyr Met  
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln  
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn  
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala  
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu  
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro  
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys  
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys  
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg  
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln  
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala  
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala  
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr  
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro  
215 220 225

Pro Gly Arg Pro Gly Gly Gly Glu Met Glu Asn Thr Leu Gln  
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser  
245 250 255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala  
260 265 270

Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala  
275 280 285

Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys  
290 295 300

Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro  
305 310 315

Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr  
320 325 330

Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile  
335 340 345

Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala  
350 355 360

Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu  
365 370 375

Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly  
380 385 390

Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu  
395 400 405

Val

<210> 147  
<211> 2052  
<212> DNA  
<213> Homo sapiens

<400> 147  
gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcct 50  
ccgctcacgc agaggctctc cgtggcttcc gcacacctgag cattaggcca 100  
gttctcctct tctctcta at ccatccgtca cctctcctgt catccgtttc 150  
catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
ttggttctga gtctcctcaa gctggatca gggcagtggc aggtgtttgg 250  
gccagacaag cctgtccagg ccttgggtgg ggaggacgca gcattctcct 300  
gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350  
aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
gccatattatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450  
attctattgc ggaggggcgc atctctgtga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccaagt cttactacca 550  
gaaggccatc tggagctac aggtgtcagc actgggctca gttcctctca 600  
tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650  
tcgggctggc tccccggcc cacagcgaag tgaaaggcacaaggaca 700  
ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgttg 750  
atgtggagat ctctctgacc gtccaagaga acgccggag catatcctgt 800  
tccatgcggc atgctcatct gagccgagag gtggaatcca gggtacagat 850  
aggagatacc ttttcgagc ctatatcgta gcacctggct accaaagtac 900  
tggaaatact ctgctgtggc ctatttttg gcattgttgg actgaagatt 950  
ttcttctcca aattccagtg gaaaatccag gcggaaactgg actggagaag 1000  
aaagcacgga caggcagaat tgagagacgc ccggaaacac gcagtggagg 1050  
tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg 1100  
aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150  
gagatttaca aggaagagtg tggggcttc tcagagttc caagcaggga 1200  
aacattactg ggaggtggac ggaggacaca ataaaaggta ggcgtggga 1250  
gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgcctcc 1300  
cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
cattaaatcc ccgttttatac agcgtcttcc ccaggacccc acctacaaaa 1400  
ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450  
aaatgaccag tcccttattt ataccctgac atgtcggtt gaaggcttat 1500  
tgagggcccta cattgagtagt ccgtcctata atgagcaaaa tggaaactccc 1550  
atagtcatct gcccagtcac ccaggaatca gagaaagagg cctcttggca 1600  
aaggccctct gcaatcccaag agacaagcaa cagtgagtc tcctcacagg 1650  
caaccacgccc cttccctcccc aggggtgaaa tgtaggatga atcacatccc 1700  
acattcttct ttagggatataaaggtctct ctcccaagatc caaagtcccg 1750  
cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800  
atgggagtca ggtgtcatgg ctggccctgag ctgggaggga agaaggctga 1850  
cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900  
ccacccctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000  
acagagtgtt tcctaattgg ttttcattt tattacactt tcagtaaaaa 2050  
aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly  
1 5 10 15

Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala  
20 25 30

Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys  
35 40 45

Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe  
50 55 60

Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe  
65 70 75

Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp  
80 85 90

Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr  
95 100 105

Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser  
110 115 120

Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly  
125 130 135

Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile  
140 145 150

Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala  
155 160 165

Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg  
170 175 180

Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu  
185 190 195

Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His  
200 205 210

Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp  
215 220 225

Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr	His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149  
<211> 24

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 149  
gcgtggtcca cctctacagg gacg 24

<210> 150  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 150  
ggaactgacc cagtgctgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 151  
gcagatgcc a cgtatcaag gcaggacaaa actggtaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
gcgatggtgc gcccgggtggc ggtggcgccg gcgggtgcgg aggcttcctt 50  
ggtcggattt caacgaggag aagatgactg accaaccgac tggctgaatg 100  
aatgaatggc ggagccgagc gcccatttag gggctggccg agcctggcg 150  
gcctcgccct gtttgtctgc gcccggccg ccggccgggt cgccctcagcc 200  
gcctcgccgg ggaatgtcac cggtgccggc gggccggcg ggcaggtgga 250  
cgcgatcgccg ggccccgggt tgccggcgaa gcccagccac cccttcctta 300  
gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350  
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctctt tggcgactg ctggaccctc ttccaccacc tttcaggcgc 450  
cgctcgcccc ctcgccgacc accccctccgg cgccggaacg cacttcgacc 500  
acctctcagg cgccgaccag acccgccgccc accacccttt cgacgaccac 550  
tggcccgccg ccgaccaccc ctgttagcgac caccgtaccg gcgcac 600  
ctccccggac cccgaccccc gatctccccca gcagcagcaa cagcagcgtc 650  
ctccccaccc cacctgccac cgaggcccccc tcttcgcctc ctccagagta 700  
tgtatgtaac tgctctgtgg ttgaaagcct gaatgtaat cgctgcaacc 750  
agaccacagg gcagtgtgag tgtcgccag gttatcaggg gcttcactgt 800  
gaaacctgca aagaggcctt ttacctaaat tacacttctg ggctctgtca 850  
gccatgtgac tgttagtccac atggagctct cagcataccg tgcaacaggt 900  
aagcaacaga gggtggaaact gaagtttatt ttatTTAGC aaggaaaaaa 950  
aaaaggctgc tactctcaag gaccatactg gtttaaacaaggaggatga 1000  
gggtcataga tttacaaaat attttatata cttttattct cttaactttat 1050  
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatTTAGT 1100  
tcttcaaaag cactagagtc gccaattttt ctctggata atttctgtaa 1150  
atttcatggg aaaaaattat tgaagaataa atctgcttc tggaaaggct 1200  
ttcaggcatg aaacctgcta ggaggttag aatgttctt atgtttatta 1250  
atataccatt ggagttgag gaaatttggttt gtttggtta ttttctctc 1300  
taatcaaaaat tctacatttg tttcttgga catctaaagc ttaacctggg 1350  
ggtaccctaa tttatTTAAC tagtgtaag tagactggtt ttactctatt 1400  
taccagtaca ttttgagac caaaagtaga ttaagcagga attatctta 1450  
aactattatg ttatTTGGAG gtaatttaat ctgtggaaat aatgtactgt 1500  
tatctaagca ttgccttgt actgcactga aagtaattat tctttgaccc 1550  
tatgtgagggc acttggcttt ttgtggaccc caagtcaaaa aactgaagag 1600  
acagtattaa ataatgaaaa aaataatgac aggttatact cagtgtacc 1650  
tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttggca 1700  
agtaatttcc ttcaactgag cttgtttctt ctcaagggtt gtgtgaagat 1750  
taaatgagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800  
ctggtttggtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgtttaaga acttttagct ccttgacaaa gaagtgcctt atactttagc 1900  
actaaatatt ttaaatgctt tataaatgat attatactgt tatggaatat 1950  
tgtatcatat tgtatgttat taaaaatgta gaagaggctg ggcgcgggtgg 2000  
ctcacgcctg taatcctagc actttggag gccaggcggtgg 2050  
tgagggcagg agttcttagat gagcctggcc agcacagtga aaccccggtct 2100  
ctactaaaaa tacaaacaaa ttagctgggc gtggtggcac acacctgttag 2150  
tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200  
tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtag 2250  
agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
1									10				15	
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
						20			25				30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
		35						40				45		
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
	50							55				60		
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
			65					70				75		
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
			80						85			90		
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100			105		
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
			110					115				120		
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
			125					130				135		
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
			140					145				150		
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
			155						160			165		
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro

	170	175	180
Ala Thr Glu Ala Pro Ser Ser Pro Pro		Pro Glu Tyr Val Cys Asn	
185		190	195
Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr			
200		205	210
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys			
215		220	225
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu			
230		235	240
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro			
245		250	255
Cys Asn Arg			

<210> 154  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 154  
aactgctctg tgggttggaaag cctg 24

<210> 155  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 155  
cagtcacatg gctgacagac ccac 24

<210> 156  
<211> 38  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-38  
<223> Synthetic construct.

<400> 156  
aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157  
<211> 689  
<212> DNA  
<213> Homo sapiens

<400> 157  
tgccgcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50  
ttctggcttt ggtctcggtg cccagggccc aggccgtgtg gttggaaaga 100  
ctggaccctg agcagcttct tggccctgg tacgtgcttgc cggtggcctc 150  
ccgggaaaag ggctttCCA tggagaagga catgaagaac gtcgtggggg 200  
tgggtggtagc cctcactcca gaaaacaacc tgccggacgct gtcctctcag 250  
cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300  
ctccggatgg gtgtttgaga atccctcaat aggctgtgtc gagctctggg 350  
tgctggccac caacttcaga gactatGCCA tcatacAACAC tcaagctggag 400  
ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
agccagccag gaggccatgg ggctcttcac caagtggagc aggacccctgg 500  
gcttcctgtc acagtagcag gcccagctgc agaaggacct cacctgtgtc 550  
cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600  
gggtcctgtg acctcggcca gtgtccaccc acctcgctca gcggctcccg 650  
ggcccccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
<211> 163  
<212> PRT  
<213> Homo sapiens

<400> 158  
Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
1 5 10 15  
Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
20 25 30  
Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
35 40 45  
Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
50 55 60  
Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
65 70 75  
His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu  
95 100 105

Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile  
110 115 120

Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu  
125 130 135

Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu  
140 145 150

Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln  
155 160

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

aacagacgtt ccctcgccgc cctggcacct ctaaccaggc acatgctgct 50  
gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100  
gtaaactgct gacgatgcag agtccgtga cggtgcagga aggccgtgt 150  
gtccatgtgc cctgctcctt ctccatcccc tcgcattggct ggatttaccc 200  
tggcccaagta gttcatggct actggttccg ggaaggggcc aatacagacc 250  
aggatgctcc agtggccaca aacaacccag ctccggcagt gtgggaggag 300  
actcgggacc gattccaccc cttggggac ccacatacca agaattgcac 350  
cctgagcatc agagatgccca gaagaagtga tgcggggaga tacttcttc 400  
gtatggagaa aggaagtata aaatggaaatt ataaacatca ccggctctct 450  
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
cctggagtcc ggctgcccccc agaatctgac ctgctctgtc ccctgggcct 550  
gtgagcaggg gacacccct atgatctccct ggataggac ctccgtgtcc 600  
ccccctggacc cctccaccac ccgctcctcg gtgctcaccc tcataccaca 650  
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700  
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750  
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800  
cttggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850  
tggctctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900  
ctgagctgga gaggcctgac cctgtcccc tcacagccct caaacccggg 950

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000  
gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050  
ctgcagagca aagccacatc aggagtact cagggggtgg tcgggggagc 1100  
tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcggttag 1150  
tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtggagat 1200  
acgggcatag agatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250  
cctgactgaa ccttggcag aagacagtcc cccagaccag cctccccag 1300  
cttctgcccgc ctcctcagtg ggggaaggag agctccagta tgcatccctc 1350  
agcttccaga tggtaagcc ttggactcg cggggacagg aggccactga 1400  
caccgagtagtc agatccacag atgagaaact gcagagactc 1450  
accctgattt agggatcaca gcccctccag gcaagggaga agtcagaggc 1500  
tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550  
atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600  
tcaaacctga atccacactg tgccctccct tttatTTTT taactaaaag 1650  
acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1									10					15

Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
					20				25					30

Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45

Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60

Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75

Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
					80				85					90

Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105

Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

110	115	120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu		
125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile		
140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser		
155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp		
170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser		
185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser		
200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn		
215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr		
230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly		
245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu		
260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu		
275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser		
290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala		
305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln		
320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val		
335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe		
350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys		
365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu		
380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala  
410 415 420

Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser  
425 430 435

Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu  
440 445 450

Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg  
455 460

<210> 161

<211> 739

<212> DNA

<213> Homo sapiens

<400> 161

gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50

accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100

cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150

tcgataagga ct当地ccggag gacaggaggc ccaggaaggt gtccccagtg 200

aaggtgacag ccctggggcg tgggaagttg gaagccacgt tcaccttcac 250

gagggaggat cggtgcattc agaagaaaat cctgatgcgg aagacggagg 300

agcctggcaa atacagcgcc tatggggca ggaagctcat gtacctgcag 350

gagctgccc a ggagggacca ctacatctt tactgcaaag accagcacca 400

tggggccctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450

accgggaggc cctggaagaa tttaagaaat tggtgacgcg caagggactc 500

tcggaggagg acatttcac gcccctgcag acgggaagct gcgttcccga 550

acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600

acacagagcc cggaccacct ggacctaccc tccagccatg accctccct 650

gctcccaccc acctgactcc aaataaagtc ctttcccccc aaaaaaaaaa 700

aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162

<211> 170

<212> PRT

<213> Homo sapiens

<400> 162

Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
1 5 10 15

Leu Ser Phe Thr Leu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20	25	30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg		
35	40	45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly		
50	55	60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile		
65	70	75
Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr		
80	85	90
Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro		
95	100	105
Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly		
110	115	120
Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr		
125	130	135
Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys		
140	145	150
Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser		
155	160	165
Cys Val Pro Glu His		
170		

<210> 163  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 163  
ggagatgaag accctgttcc tg 22

<210> 164  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 164  
ggagatgaag accctgttcc tgggtg 26

<210> 165  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct.

<400> 165  
gtcctccgga aagtccatat c 21

<210> 166  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 166  
gcctagtgtt cgggAACGCA gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 167  
caggcacctg gtacgtaaag gccatggtgg tcgataagga ctttccggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 168  
ctgtccattca ccctggagga ggaggatatc acagggaccc ggtac 45

<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169

gttccgcaga tgcagagggtt gaggtggctg cgggactgga agtcatcg 50  
cagaggtctc acagcagcca aggaacctgg ggcccgcctcc tccccctcc 100  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150  
gtagggggag agaccaggat catcaagggg ttgcagtgca agcctcactc 200  
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250  
cgacgctcat cgcccccaga tggctcctga cagcagccca ctgcctcaag 300  
ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350  
ctgtgagcag acccggacag ccactgagtc cttcccccac cccggcttca 400  
acaacagcct ccccaacaaa gaccaccgca atgacatcat gctggtgaag 450  
atggcatcgc cagtctccat cacctggct gtgcgacccc tcaccctctc 500  
ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550  
gcacgtccag cccccagttt cgcctgcctc acaccttgcg atgcgccaac 600  
atcaccatca ttgagcacca gaagtgttag aacgcctacc ccggcaacat 650  
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700  
gccagggtga ctccgggggc cctctggct gtaaccagtc tcttcaaggc 750  
attatctcct ggggccagga tccgtgtgcg atcaccogaa agcctggtgt 800  
ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850  
acaatttagac tggacccacc caccacagcc catcaccctc catttccact 900  
tggtgtttgg ttccctgttca ctctgttaat aagaaacctt aagccaagac 950  
cctctacgaa cattcttgg gcctcctgg ctacaggaga tgctgtcact 1000  
taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050  
ccttgaataa ttgtgactct gggaatgaca acacctgggt tggctctgt 1100  
tgtatccccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150  
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200  
aaaa 1204

<210> 170  
<211> 250  
<212> PRT  
<213> Homo sapiens

<400> 170  
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu  
1 5 10 15

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro
				20				25					30	
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu
				35				40					45	
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala
				50				55					60	
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His
				65				70					75	
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr
				80				85					90	
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys
				95				100					105	
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val
				110				115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys
				125				130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr
				140				145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn
				155				160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly
				170				175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly
				185				190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn
				200				205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala
				215				220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val
				230				235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn					
				245				250						

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171  
ggctgcggga ctggaagtca tcggg 25

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 172  
ctccaggcca tgaggattct gcag 24

<210> 173  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 173  
cctctggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 174  
tctgtatgt tgccgggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 175  
cgttagaca ccaggtttc gggtg 25

<210> 176  
<211> 18  
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176  
cccttgatga tcctggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178  
gagagaccag gatcatcaag gggttcgagt gcaaggctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179  
gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50  
gattcattgt tttcttttat ctgtggggcc ttttactgc tcagagacaa 100  
aagaaaagagg agagcaccca agaagtgaaa atagaagttt tgcatcgcc 150  
agaaaaactgc tctaagacaa gcaagaaggg agacctacta aatgccatt 200  
atgacggcta cctggctaaa gacggctcgaa aattctactg cagccggaca 250  
caaaaatgaag gccaccccaa atggttgtt cttgggtttg ggcaagtcat 300  
aaaaggccta gacattgcta tgacagatgtgtt gaaaggcggaa 350  
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcggaa 400

ggcaagattc caccggatgc tacattgatt tttgagattt aactttatgc 450  
tgtgaccaaa ggaccacgga gcattgagac atttaaacaa atagacatgg 500  
acaatgacag gcagctctc aaagccgaga taaacctcta cttgcaaagg 550  
gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600  
tttagaagat attttaaga agaatgacca tgatggtgat ggcttcattt 650  
ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700  
atttctactt tttttttta gctatttact gtactttatg tataaaaacaa 750  
agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800  
tttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850  
ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900  
aaaaaaaa 907

<210> 180

<211> 222

<212> PRT

<213> Homo sapiens

<400> 180

Met	Pro	Lys	Thr	Met	His	Phe	Leu	Phe	Arg	Phe	Ile	Val	Phe	Phe
1														15

Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu
														30

Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn
														45

Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr
														60

Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg
														75

Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly
														90

Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro
														105

Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly
														120

Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu
														135

Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser
														150

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu  
155 160 165

Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys  
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu  
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser  
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu  
215 220

<210> 181

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 182

gacatggaca atgacagg 18

<210> 183

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 183

cctttcagga tgtaggag 18

<210> 184

<211> 18

<212> DNA

<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 184  
gatgtctgcc accccaag 18

<210> 185  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-27  
<223> Synthetic construct.

<400> 185  
gcatcctgat atgacttgac acgtggc 27

<210> 186  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 186  
tacaagaggg aagaggagg 24

<210> 187  
<211> 52  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-52  
<223> Synthetic construct.

<400> 187  
gcccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188  
<211> 573  
<212> DNA  
<213> Homo sapiens

<400> 188  
cagaaatgca gggaccattg cttttccag gcctctgctt tctgctgagc 50  
ctctttggag ctgtgactca gaaaacccaaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150  
ataacttctgg atctggcag aaactattca cattcccctt ggagacatgt 200  
aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250  
aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300  
atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtgg 350  
ggtgcatgcc tgcaatccca gttactcggg aggctgagggc aggagaatcg 400  
cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450  
ctccagcatg gatgacagag caagactccg tctaaaaaag aaaagatagt 500  
ttcttgtttc atttcgcgac tgccctctca gtgttcctg ggatcccctc 550  
ccaaataaaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5			10						15	
Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
	20						25						30	
Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
		35						40					45	
Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
		50						55					60	
Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu	
				65					70					

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 192  
cctgtgctaa gtgcccccc aatgcttcct gtgtcaataa cactcaactgc 50

<210> 193  
<211> 1091  
<212> DNA  
<213> Homo sapiens

<400> 193  
caagcaggc atccccttgg tgaccttcaa agagaagcag agagggcaga 50  
ggtggggggc acagggaaag ggtgacctct gagattcccc tttccccc 100  
gactttggaa gtgaccaccatgggctca gcatctttt gctcctgtgt 150  
gttottggc tcagccaggc agccacaccg aagatttca atggcactga 200  
gtgtggcgt aactcacagc cgtggcaggt ggggctgtt gagggcacca 250  
gcctgcgtg cgggggtgtc ttattgacc acaggtgggt cctcacagcg 300  
gctcaactgca gcggcagcag gtactgggt cgcctgggg aacacagcct 350  
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
cccatcccggtt ctagctggaa gcctcgacga gccacgagca cgacctccgg 450  
ctgtgcggc tgcgcctgcc cgtccgcgtt accagcagcg ttcaacccct 500  
gccccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550  
gctggggcat caccaaccac ccacggaaacc cattcccgga tctgctccag 600  
tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650  
cgggagaatc acgagcaaca tggtgtgtgc aggccggcgtc cgggggcagg 700  
atgcctgcca gggtgattct gggggccccc tggtgtgtgg gggagtcctt 750  
caaggtctgg tgtcctgggg gtctgtggg cccctgtggac aagatggcat 800

ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850  
tcatgaggaa caactgaccc gtttcctcca cctccacccc cacccctaa 900  
cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950  
ccctagctcc actcttggtg gcctggaaac ttcttggAAC tttaactcct 1000  
gccagccctt ctaagaccca cgagcgggt gagagaagtg tgcaatagtc 1050  
tggaataaat ataaatgaag gagggcAAA aaaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser
1										10				15
Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg														
										25				30
Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu														
										35				45
Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala														
										50				60
Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His														
										65				75
Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly														
										80				90
Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His														
										95				105
Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val														
										110				120
Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr														
										125				135
Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His														
										140				150
Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser														
										155				165
Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile														
										170				180
Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala														
										185				195
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu														

200	205	210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp		
215	220	225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp		
230	235	240
Ile Arg Met Ile Met Arg Asn Asn		
245		

<210> 195

<211> 1485

<212> DNA

<213> Homo sapiens

<400> 195

gcggccacac gcagctagcc ggagccccgga ccaggcgccct gtgccttcctc 50  
 ctcgtccctc gcccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100  
 tcgcacatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150  
 ggcttgctca aagcccgca ggagaggagg ctggccgaga tcaaccggga 200  
 gtttctgtgt gaccagaagt acagtgtatga agagaacctt ccagaaaaagc 250  
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300  
 gagattgacc ttagtgtctt aaagaggatg atggagaagc ttgggtgtccc 350  
 caagacccac ctggagatga agaagatgat ctcagaggtg acaggagggg 400  
 tcagtgacac tatatacctac cgagactttg tgaacatgtat gctggggaaa 450  
 cggtcggctg tcctcaagtt agtcatgtat tttgaaggaa aagccaacgaa 500  
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550  
 tgccctgagg accccgcctg gactccccag cttcccacc ccataacctcc 600  
 ctccccatct tgctgccctt cttgacacac tgtatctct ctctctctca 650  
 tttgttttgtt cattgagggt ttgtttgtgt tttcatcaat gtctttgtaa 700  
 agcacaaaatt atctgcctta aaggggctct gggtcggggaa atcctgagcc 750  
 ttgggtcccc tccctctctt cttccctctt tccccgcctcc ctgtgcagaa 800  
 gggctgatataaaactagaggggg gcagggccag ggcaggagg 850  
 cttccagcct gtgtccctt cacttggagg aaccagcact ctccatcctt 900  
 tcagaaaatc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950  
 gaccccaaggc cactctgaga agaccttggaa gtagggacaa ggctgcaggg 1000  
 cctcttcgg gtttccttgg acagtgccat gttccagtg ctctgggtgtc 1050

acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100  
attccacacc tcttctcatc ctcagtatg tgaaggtggg aaggaaagga 1150  
gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200  
ctgcctcttg gccacacccctg tgcaaggcagc tgagaggcag cgtgcagccc 1250  
tactgtccct tactggggca gcagaggcgt tcggaggcag aagtgaggcc 1300  
tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350  
gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400  
aagtcafcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450  
tgaccccaat ctgcttggaaa aaaaaaaaaaaaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe
1				5					10					15

Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
			20					25						30

Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
			35					40						45

Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
			50					55						60

Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
			65					70						75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
			80					85						90

Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
			95					100						105

Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
			110					115						120

Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
			125					130						135

Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
			140					145						150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

cgcgtcccc gcgcgcctcc tcgggctcca cgcgtctgc cccgcagagg 50  
cagccttcctc caggagcggg gccctgcaca ccatggcccc cgggtggca 100  
ggggtcggcg ccgcgcgtgcg cgccgcctg ggcgtggct tggcgctggc 150  
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200  
gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgccgttcct 250  
cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataat 300  
caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350  
tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccctccag 400  
gacctgaagc agcttagagcg actgcgcctg aacaagaata agctgcaagt 450  
ccttccagaa ttgcgtttcc agagcacgcc gaagctcacc agactagatt 500  
tgagtgaaaa ccagatccag gggatcccga ggaaggcggt ccgcggcatc 550  
accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600  
agatggagcc ttccgagcgc tgcgcattt ggagatcctt accctaaca 650  
acaacaacat cagtcgcatc ctggtcacca gcttcaacca catgccgaag 700  
atccgaactc tgccctcca ctccaaccac ctctactgcg actgccacct 750  
ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca 800  
cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggccgatgtg 850  
cagaagaagg agtacgtgtg cccagcccc cactcgagc ccccatcctg 900  
caatgccaac tccatctcct gcccttcgcc ctgcacgtgc agcaataaca 950  
tcgtggactg tcgagggaaag ggcttgatgg agattcctgc caacttgccg 1000  
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 1050  
tgcaggagcc ttcacccagt acaagaaact gaagcgaata gacatcagca 1100  
agaatcagat atcggatatt gctccagatg cttccaggg cctgaaatca 1150  
ctcacatcgc tggcctgtta tggaaacaag atcaccgaga ttgccaagg 1200  
actgtttgtt gggctgggtt ccctacagct gctcctcctc aatgccaaca 1250  
agatcaactg cctgcgggtg aacacgttgc aggacctgca gaacctcaac 1300  
ttgctctccc tgtatgacaa caagctgcag accatcagca aggggctt 1350  
cgccccctcg cagtccatcc agacactcca cttagcccaa aaccctttg 1400  
tgtgcgactg ccacttgaag tggctggccg actacactcca ggacaacccc 1450

atcgagacaa gcggggcccg ctgcagcagc ccgcgccgac tcgccaacaa 1500  
gcgcatcagc cagatcaaga gcaagaagtt ccgctgctca ggctccgagg 1550  
attaccgcag caggttcagc agcgagtgt tcataggacct cgtgtcccc 1600  
gagaagtgtc gctgtgaggg cacgattgtg gactgctcca accagaagct 1650  
ggtccgcata ccaagccacc tccctgaata tgtcaccgac ctgcgactga 1700  
atgacaatga ggtatctgtt ctggaggcca ctggcatctt caagaagttg 1750  
cccaacactgc ggaaaataaa tctgagtaac aataagatca aggaggtgcg 1800  
agagggagct ttgcgtggag cagccagcgt gcaggagctg atgctgacag 1850  
ggaaccagct ggagaccgtg cacgggcgcg tgttccgtgg cctcagtggc 1900  
ctcaaaacct ttagtgcgtg gagtaacttg atcagctgtg tgtagtaatga 1950  
caccttgcgc ggcctgagtt cggtgagact gctgtccctc tatgacaatc 2000  
ggatcaccac catcaccctt gggccttca ccacgcttgt ctccctgtcc 2050  
accataaacc tcctgtccaa ccccttcaac tgcaactgcc acctggcctg 2100  
gctcggcaag tgggtgagga agaggcggat cgtcagtggg aaccctaggt 2150  
gccagaagcc attttccctc aaggagattc ccatccagga tgtggccatc 2200  
caggacttca cctgtgtatgg caacgaggag agtagctgcc agctgagccc 2250  
gcgcgtcccg gagcagtgca cctgttatgga gacagtggtg cgatgcagca 2300  
acaaggggct ccgcgcctc cccagaggca tgcccaagga tgtgaccgag 2350  
ctgtacctgg aaggaaacca cctaacagcc gtgcccagag agctgtccgc 2400  
cctccgacac ctgacgctta ttgacctgag caacaacagc atcagcatgc 2450  
tgaccaatta caccttcaagt aacatgtctc acctctccac tctgatcctg 2500  
agctacaacc ggctgaggtg catccccgtc cacgccttca acgggctgcg 2550  
gtccctgcga gtgctaacc tccatggcaa tgacatttcc agcgttccctg 2600  
aaggctcctt caacgacctc acatctcttt cccatctggc gctggaaacc 2650  
aacccactcc actgtgactg cagtcttcgg tggctgtcgg agtgggtgaa 2700  
ggcgggtac aaggagcctg gcatcgcccg ctgcagtagc cctgagccca 2750  
tggctgacag gctcctgctc accaccccaa cccaccgctt ccagtgc当地 2800  
ggcccaatggg acatcaacat tgtggccaaa tgcaatgcct gcctctccag 2850  
cccggtcaag aataacggga catgcaccca ggaccctgtg gagctgtacc 2900

gctgtgcctg cccctacagc tacaaggca aggactgcac tgtgcccattc 2950  
aacacctgca tccagaaccc ctgtcagcat ggaggcacct gccacctgag 3000  
tgacagccac aaggatgggt tcagctgctc ctgccctctg ggctttgagg 3050  
ggcagcggtg tgagatcaac ccagatgact gtgaggacaa cgactgcgaa 3100  
aacaatgcca cctgcgtgga cggatcaac aactacgtgt gtatctgtcc 3150  
gcctaactac acaggtgagc tatgcacga ggtgattgac cactgtgtgc 3200  
ctgagctgaa cctctgtcag catgaggcca agtgcacccc cctggacaaa 3250  
ggattcagct gcgagtgtgt ccctggctac agcgggaagc tctgtgagac 3300  
agacaatgat gactgtgtgg cccacaagtg cgcacacggg gcccagtgcg 3350  
tggacacaat caatggctac acatgcaccc gcccccaggg cttcagtgga 3400  
cccttctgtg aacacccccc acccatggtc ctactgcaga ccagcccatg 3450  
cgaccagtac gagtgccaga acggggccca gtgcacgtg gtgcagcagg 3500  
agcccacctg ccgctgcca ccaggcttcg ccggcccccag atgcgagaag 3550  
ctcatcactg tcaacttcgt gggcaaagac tcctacgtgg aactggcctc 3600  
cgccaaggtc cgaccccagg ccaacatctc cctgcaggtg gccactgaca 3650  
aggacaacgg catccttctc tacaaggag acaatgaccc cctggcactg 3700  
gagctgtacc agggccacgt gcggctggc tatgacagcc ttagttcccc 3750  
tccaaccaca gtgtacagt tggagacagt gaatgatggg cagttcaca 3800  
gtgtggagct ggtgacgcta aaccagaccc tgaacctagt agtggacaaa 3850  
ggaactccaa agagcctggg gaagctccag aagcagccag cagtggcat 3900  
caacagccccc ctctacccctg gaggcatccc cacctccacc ggcctctccg 3950  
ccttgcgcca gggcacggac cggcctctag gcggcttcca cggatgcattc 4000  
catgaggtgc gcatcaacaa cgagctgcag gacttcaagg ccctcccacc 4050  
acagtccctg ggggtgtcac caggctgcaa gtcctgcacc gtgtgcaagc 4100  
acggcctgtg ccgctccgtg gagaaggaca gcgtgggtgtg cgagtgcgcgc 4150  
ccaggctgga ccggcccaact ctgcgaccag gaggccggg acccctgcct 4200  
cgccccacaga tgccaccatg gaaaatgtgt ggcaactggg acctcataca 4250  
tgtgcaagtg tgccgagggc tatggagggg acttgtgtga caacaagaat 4300  
gactctgcca atgcctgctc agccttcaag tgtcaccatg ggcagtgcct 4350

catctcagac caaggggagc cctactgcct gtgccagccc ggcttagcg 4400  
gcgagcactg ccaacaagag aatccgtgcc tggacaagt agtccgagag 4450  
gtgatccgcc gccagaaagg ttatgcatca tgtgccacag cctccaaggt 4500  
gcccatcatg gaatgtcgtg gggctgtgg gccccagtgc tgccagccca 4550  
cccgcagcaa gcggcggaaa tacgtttcc agtgcacgga cggctcctcg 4600  
ttttagaag aggtggagag acacttagag tgcggctgcc tcgcgtgttc 4650  
ctaagccct gcccgcctgc ctgccaccc tcggactcca gcttgatgga 4700  
gttggacag ccatgtggaa cccctggtg attcagcatg aaggaaatga 4750  
agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800  
aaacaaaaaa tagaactaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg
1				5					10				15	

Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro
				20					25				30	

Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val
			35					40					45	

Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro
				50				55					60	

Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg
				65				70					75	

Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu
			80					85					90	

His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe
				95				100					105	

Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys
				110				115					120	

Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu
				125				130					135	

Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg
				140				145					150	

Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp
				155				160					165	

Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu
														180
														175
														170
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Ile	Ser	Arg	
														195
														190
														185
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu
														210
														205
														200
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp
														225
														220
														215
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr
														240
														235
														230
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp
														255
														250
														245
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro
														270
														265
														260
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr
														285
														280
														275
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu
														300
														295
														290
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu
														315
														310
														305
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr
														330
														325
														320
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp
														345
														340
														335
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu
														360
														355
														350
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe
														375
														365
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys
														390
														385
														380
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu
														405
														400
														395
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys
														420
														415
														410
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala
														435
														425
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp
														450
														445
														440
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser

455	460	465
Ser Pro Arg Arg Leu Ala Asn Lys Arg Ile Ser Gln Ile Lys Ser		
470	475	480
Lys Lys Phe Arg Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe		
485	490	495
Ser Ser Glu Cys Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg		
500	505	510
Cys Glu Gly Thr Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg		
515	520	525
Ile Pro Ser His Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn		
530	535	540
Asp Asn Glu Val Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys		
545	550	555
Leu Pro Asn Leu Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys		
560	565	570
Glu Val Arg Glu Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu		
575	580	585
Leu Met Leu Thr Gly Asn Gln Leu Glu Thr Val His Gly Arg Val		
590	595	600
Phe Arg Gly Leu Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn		
605	610	615
Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser		
620	625	630
Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr		
635	640	645
Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu		
650	655	660
Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly		
665	670	675
Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys		
680	685	690
Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala		
695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln		
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val		
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met		
740	745	750

Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr  
 755 760 765  
 Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile  
 770 775 780  
 Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe  
 785 790 795  
 Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg  
 800 805 810  
 Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu  
 815 820 825  
 Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu  
 830 835 840  
 Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly  
 845 850 855  
 Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu  
 860 865 870  
 Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser  
 875 880 885  
 Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr  
 890 895 900  
 His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala  
 905 910 915  
 Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr  
 920 925 930  
 Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr  
 935 940 945  
 Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile  
 950 955 960  
 Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser  
 965 970 975  
 His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly  
 980 985 990  
 Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys  
 995 1000 1005  
 Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys  
 1010 1015 1020  
 Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile  
 1025 1030 1035  
 Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys

	1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly			
1055	1060	1065	
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala			
1070	1075	1080	
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly			
1085	1090	1095	
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu			
1100	1105	1110	
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln			
1115	1120	1125	
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu			
1130	1135	1140	
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu			
1145	1150	1155	
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu			
1160	1165	1170	
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln			
1175	1180	1185	
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp			
1190	1195	1200	
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu			
1205	1210	1215	
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val			
1220	1225	1230	
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr			
1235	1240	1245	
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys			
1250	1255	1260	
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser			
1265	1270	1275	
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala			
1280	1285	1290	
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys			
1295	1300	1305	
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala			
1310	1315	1320	
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys			
1325	1330	1335	

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser  
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp  
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly  
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu  
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn  
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser  
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly  
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg  
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala  
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln  
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln  
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu  
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser  
1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 200  
ttgttggcat tgaggaggag cagc 24

<210> 201  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 201  
gagggcatcg tcgaaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202  
<211> 753  
<212> DNA  
<213> Homo sapiens

<400> 202  
ggatgcagga cgctccctg agctgcctgt caccgactag gtggagcagt 50  
gtttttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100  
gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150  
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200  
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
caattactgg ggcttcagcc ttggaaactg gatctgcattt gcatattatg 300  
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350  
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400  
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500  
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
cctgtccgag tggaaaaaaag gctgtgaggt ttcctaaact ggaactggac 600  
ccaggatgct ttgcagcaac gcccttaggat ttgcagtcaa tgtccaaatg 650  
cctgtgtcat cttgtccccgt ttccctccaa tattccttct caaacttgga 700  
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaaat 750  
gtc 753

<210> 203  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 203  
Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr  
1 5 10 15  
  
Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile  
20 25 30  
  
Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly  
35 40 45  
  
Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr  
50 55 60  
  
Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe  
65 70 75  
  
Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu  
80 85 90  
  
Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp  
95 100 105  
  
Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr  
110 115 120  
  
Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
125 130 135  
  
Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
140 145

<210> 204  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 204  
gcaggcttg aggatgaagg ctgc 24

<210> 205  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 205  
ctcattggct gcctggtcac aggc 24

<210> 206  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 206  
ccagtcggac aggtctctcc cctc 24

<210> 207  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 207  
tcagtgacca aggctgagca ggcg 24

<210> 208  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 208  
ctacactcgt tgcaaactgg caaaaatatt ctcgagggtt ggcctgg 47

<210> 209  
<211> 1648  
<212> DNA  
<213> Homo sapiens

<400> 209  
caggccattt gcatcccact gtccttgtgt tcggagccag gccacaccgt 50  
cctcagcagt gtcatgtgtt aaaaacgcca agctgaatat atcatgcccc 100  
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
ctttttacct tggtgtctgc ctgtatccca gtgttcaggc tggcttagacg 200  
gcggaagaag atccttatattt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300  
gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350  
cacagctgct gttttaagg aaacattcaa gtccctgtct cacatagacc 400  
ctgatgtcct ctatccatct ctaaatgtca ccagcttga ctcagttgtt 450  
cctgaaaagc tggatgacct agtccccaaag gggaaaaaat tcctgctgct 500  
ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550  
ccctagtaca gctgcgtgga agattgacat cccaagattg ggagagggtt 600  
catctgatcg tggcaggtgg ttatgacgag agagtccctgg agaatgtgga 650  
acattatcag gaattgaaga aaatggtcca acagtccgac cttggccagt 700  
atgtgacctt cttgaggtct ttctcagaca aacagaaaaat ctccttcctc 750  
cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800  
tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850  
cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900  
gagcctgacc cggtgcactt ctcagaagca atagaaaaagt tcacccgtga 950  
accttcctta aaagccacca tggcctggc tggaaagagcc agagtgaagg 1000  
aaaaattttc ccctgaagca tttacagaac agctctaccg atatgttacc 1050  
aaactgctgg tataatcaga ttgttttaa gatctccatt aatgtcattt 1100  
ttatggattg tagaccagt ttgaaacca aaaaagaaac ctagaatcta 1150  
atgcagaaga gatctttaa aaaataaact tgagtcttga atgtgagcca 1200  
ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250  
tttatgctat aatcattcca aatttgcca gtgttaagtt acaaatgtgg 1300  
tgtcattcca tggcctggc agtattttaa ttatattttc tcgggattat 1350  
tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggtttc 1400  
atagtttaag tgtgtatcat tatcaaagtt gattaatttgc gcttcatagt 1450  
ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500  
tcactgtcat ctgttaggga atttttgcatt gtcctgtctt tgcctggatc 1550  
catagcgaga gtgctctgta tttttttaa gataatttgcatttgcac 1600  
actgagat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210  
<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	
1				5					10				15		
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	
				20				25				30			
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	
				35				40				45			
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	
				50				55				60			
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	
				65				70				75			
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	
				80				85				90			
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	
				95				100				105			
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	
				110				115				120			
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	
				125				130				135			
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	
				140				145				150			
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	
				155				160				165			
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	
				170				175				180			
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	
				185				190				195			
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	
				200				205				210			
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	
				215				220				225			
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	
				230				235				240			
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	
				245				250				255			
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	
				260				265				270			

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg  
275 280 285  
Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg  
290 295 300  
Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr  
305 310 315  
Arg Tyr Val Thr Lys Leu Leu Val  
320

<210> 211  
<211> 1554  
<212> DNA  
<213> Homo sapiens

<400> 211  
gactacgccc atccgagacg tggctccctg ggccggcagaa ccatgttgga 50  
cttcgcgatc ttgcgcgtta ccttcttgct ggcggtggtg ggagccgtgc 100  
tctacacctta tccggcttcc agacaagctg caggaattcc agggattact 150  
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaaag 200  
tttgcatgag ttcctggtta atttgcatga gagatatggg cctgtggtct 250  
ccttctggtt tggcaggcgc ctgcgtggta gtttggcac tggatgtgt 300  
ctgaaggcgc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350  
gctgaagtca ttatataaggat atcaatctgg tggtggcagt gtgagtgaaa 400  
accacatgag gaaaaaaattt tatggaaaatg gtgtgactga ttctctgaag 450  
agtaactttg ccctcctcct aaagcttca gaagaattat tagataaatg 500  
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgctt 550  
gttttgcata gaagtctgtt acacagatgg taatggtag tacatggaa 600  
gatgatcagg aagtcatcg cttccagaag aatcatggca cagttggtc 650  
tgagatttggaa aaaggcttca tagatgggtc acttgataaa aacatgactc 700  
ggaaaaaaaca atatgaagat gccctcatgc aactggagtc tggttttaagg 750  
aacatcataa aagaacgaaa aggaaggaac ttcaatcaac atatttcat 800  
tgactcctta gtacaaggaa acctaataatga ccaacagatc ctagaagaca 850  
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
tgggcaatct gtttttaac cacctctgaa gaagttcaaa aaaaattata 950  
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050  
gccaaactga ctccagttc tgcccagctt caagatattg aaggaaaaat 1100  
tgaccgattt attattccta gagagaccct cgtccttat gcccttggtg 1150  
tggtaacctca ggatccta atctggccat ctccacacaa gtttgatcca 1200  
gatcggtttg atgatgaatt agtaatgaaa acttttcct cacttggatt 1250  
ctcaggcaca caggagtgtc cagagttgag gtttgcata atgggtacca 1300  
cagtaaccttct tagtgtattt gtgaagagac tgcacctact ttctgtggag 1350  
ggacaggta ttgaaacaaa gatgaaactg gtaacatcat caagggaga 1400  
agcttggatc actgtctcaa agagatatta aaattttata catttaaat 1450  
cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgtt 1500  
aatcctttta taaaccagta tcactttgtatataaacac ctatttgta 1550

ttaa 1554

<210> 212  
<211> 462  
<212> PRT  
<213> Homo sapiens

<400> 212  
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu  
1 5 10 15  
Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala  
20 25 30  
Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu  
35 40 45  
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn  
50 55 60  
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg  
65 70 75  
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His  
80 85 90  
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys  
95 100 105  
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Ser Val Ser Glu Asn  
110 115 120  
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu  
125 130 135  
Lys Ser Asn Phe Ala Leu Leu Lys Leu Ser Glu Glu Leu Leu

140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser		
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val		
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln		
185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu		
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu		
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys		
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser		
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser		
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys		
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys		
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val		
305	310	315
Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu		
320	325	330
Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln		
335	340	345
Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg		
350	355	360
Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro		
365	370	375
Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp		
380	385	390
Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly		
395	400	405
Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr		
410	415	420
Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val		
425	430	435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser  
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

ctagatttgt cggcttgcgg ggagacttca ggagtcgctg tctctgaact 50  
tccagcctca gagaccgcgg cccttgcgtccc cgagggccat gggccgggtc 100  
tcagggcttg tgccctctcg ctgcctgacg ctgcctggcgc atctggtggt 150  
cgtcatcacc ttattcttgtt cccgggacag caacatacag gcctgcctgc 200  
ctctcacgtt caccccccggag gagtatgaca agcaggacat tcagctggtg 250  
gccgcgcgtct ctgtcacccct gggctcttt gcagtggagc tggccgggtt 300  
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
gggctcactg tagtgcattcc gtggccctgt cttcttcat attcgagcgt 400  
tgggagtgca ctacgtattt gtacattttt gtcttctgca gtgcccttcc 450  
agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
aacccctctg attaccttca tgacggaaac ctaaggacga agcctacagg 550  
ggcaaggggcc gcttcgtatt ccttggaaagaa ggaaggcata ggcttcgggtt 600  
ttccccctcgg aaactgcattc tgctggagga tatgtgttgg aataattacg 650  
tctttagtct gggattatcc gcattgtatt tagtgcattttaataaaaata 700  
tgtttttagt taacattaag acttatatac agtttttaggg gacaattaaa 750  
aaaaaaaaaa 759

<210> 214

<211> 140

<212> PRT

<213> Homo sapiens

<400> 214

Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
1 5 10 15  
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
20 25 30  
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
35 40 45

Tyr	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr
				50					55					60
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val
				65					70					75
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His
				80					85					90
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp
				95				100						105
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu
				110				115						120
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu
				125				130						135
Lys	Lys	Lys	Pro	Phe										
				140										

<210> 215

<211> 697

<212> DNA

<213> Homo sapiens

<400> 215

```
tcccgaccc tgccgccctg ccactatgtc cggccgcctt atgctgcttg 50
cctggctct ccccagcctc ctgcactcg gagcggctca ggagacagaa 100
gaccggcct gctgcagccc catagtgccc cgaaacgagt ggaaggccct 150
ggcatcagag tgcgcccagc acctgaggct gcccttacgc tatgtggtgg 200
tatcgacac ggcgggcagc agctgcaaca ccccccgcctc gtgccagcag 250
caggccccga atgtcagca ctaccacatg aagacactgg gctggtgca 300
cgtggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gcccactcag gtcacttatg gaacccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc aggtctact ggctgcgggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
acactctctc caggcaacca gcttaccac ctcatccaga attggccaca 600
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctccctcc 650
catggccaaa aaccccactg tctccttctc caataaagat gtagctc 697
```

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu
1					5				10					15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys
					20				25					30
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu
					35				40					45
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser
					50				55					60
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln
					65				70					75
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp
					80				85					90
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val
					95				100					105
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His
					110				115					120
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
					125				130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
					140				145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
					155				160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
					170				175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
					185				190					195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

ctggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50  
gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg caggtagcc 100  
tctatcttgtt catctgtggc caggtatgtg gtcctcccg 150  
cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcggaa 200

gcggggccac atctcaccta agtcccggcc catggccaaat tccactctcc 250  
tagggctgct ggccccgcct ggggaggcgtt ggggcattct tggcagcccc 300  
cccaaccgccc cgaaccacag ccccccaccc tcagccaagg tgaagaaaat 350  
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400  
tgctcgtcac agggaaagatt gtggaccatg gcaatgggac cttagcgtc 450  
cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500  
gccccccagt aaagctgttag agttccacca ggaacagcag atcttcatcg 550  
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600  
gaacggggcc gccggaccc tcgttgcacc cacgaccagg ccaagatctg 650  
ctcccgagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700  
tcaaagtctgt ctgtgtctac atgccttct acagcacgga ctatcgctg 750  
gtccagaagg tgtgcccaga ttacaactac catagtgata cccctacta 800  
cccatctggg tgacccgggg cagggccacag aggccaggcc agggctggaa 850  
ggacaggcct gcccattgcag gagaccatct ggacaccggg cagggaaagg 900  
gttgggcctc aggcagggag ggggtggag acgaggagat gccaagtggg 950  
gccagggcca agtctcaagt ggcagagaaa gggtcccaag tgctggtccc 1000  
aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050  
ggctctctgt gcagcctcac agggcttgc cacggagcca cagagagatg 1100  
ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150  
gtcatggag gaagctaagc cttgggttct tgccatcctg aggaaagata 1200  
gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250  
atggatggct gagagggctt cctaggagcc agtcagcagg gtgggggtggg 1300  
gccagaggag ctctccagcc ctgcctagtg ggcccccgtga gccccttgc 1350  
gtgtgctgag catggcatga ggctgaagtg gcaaccctgg ggtctttgat 1400  
gtcttgacag attgaccatc tgtctccagc caggccaccc cttccaaaa 1450  
ttccctcttc tgccagtact cccctgtac cacccattgc tcatggcaca 1500  
cccatcctta agctaagaca ggacgattgt ggtccctcca cactaaggcc 1550  
acagccccatc cgccgtgtgt gtgtccctct tccaccccaa cccctgctgg 1600  
ctcctctggg agcatccatg tcccgagag gggtccctca acagtcagcc 1650

tcacctgtca gaccggggtt ctcccgatc tggatggcgc cgccctctca 1700  
gcagcggca cgggtggggc ggggccggc cgcatgtgtcgtcgt 1750  
tgttctgtgt gtctgtctgt ggggtggggg aggggaggga agtcttgtga 1800  
aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850  
aataaagctt gccccggggc a 1871

<210> 218  
<211> 252  
<212> PRT  
<213> Homo sapiens

<400> 218  
Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser  
1 5 10 15  
Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser  
20 25 30  
Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg  
35 40 45  
Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met  
50 55 60  
Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala  
65 70 75  
Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro  
80 85 90  
Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe  
95 100 105  
Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly  
110 115 120  
Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln  
125 130 135  
His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro  
140 145 150  
Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile  
155 160 165  
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu  
170 175 180  
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro  
185 190 195  
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp  
200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219  
gtgaatgtga gggttttagatg actttcagat gtcttaggaac cagagtgggt 50  
gcagggggccc caggcagggc tgatttcttgg gcggaggaga gtagggtaaa 100  
gggttctgca tgagctccctt aaaggacaaa ggtaacagag ccagcgagag 150  
agctcgaggg gagacttga cttcaagcca cagaatttgtt ggaagtgtgc 200  
gcgcgcgcgc cgccgtcgct cctgcagcgc tgtcgaccta gccgctagca 250  
tcttcccag caccgggatc cccgggttagg aggcgacgcg ggcgagcacc 300  
agcgccagcc ggctgcggct gcccacacgg ctcaccatgg gctccggcg 350  
ccgggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400  
ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450  
aagtgtctgg tggtgtgcga ctogaacccg gccacggact ccaagggctc 500  
ctcttcctcc ccgctgggga tatcggtccg ggcggccaac tccaaggctcg 550  
ccttctcgcc ggtgcggagc accaaccacg agccatccga gatgagcaac 600  
aagacgcgca tcatttactt cgatcagatc ctggtaatg tggtaattt 650  
tttcacattt gagtctgtct ttgttagcacc aagaaaagga atttacagtt 700  
tcagtttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750  
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800  
tgttactcgt gaagctgcca cgaatgggtgt cctgctctac ctagataaag 850  
aggataaggt ttacctaaaa ctggagaaag gtaatttgtt tggaggctgg 900  
cagtttcca cgtttctgg ctttctgg tttcccttat aggattcaat 950  
ttctccatga tggatcca ggtgagggat gacccactcc ttagttattt 1000  
gaagatcatt ttttcatcat tggattgatg tcttttattt gtttctcatg 1050  
ggtgatatg gattctaagg attcttagcct gtctgaacca atacaaaatt 1100

tcacagatta tttgtgtgtg tctgtttcag tatatttggaa ttgggactct 1150  
aagcagataa tacctatgct taaaatgtAAC agtcaaaaAGC tgtctgcaag 1200  
acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250  
gaattttatt tgTTTtagTTT taaaAGACTG gcaaccaggT ctaaggatta 1300  
gaaaactcta aagttctgac ttcaatcaac ggTTAGTGTG atactGCCAA 1350  
agaactgtat actgtgttaa tatattgatt atatttgTTT ttattccTTT 1400  
ggaatttagtt tgTTTggTTC ttgtaaaaaa cttggatTTT tttttcagt 1450  
aactggtatt atgtttctc ttAAAATAAG gtaatgaatg gcttgcccac 1500  
aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaaa 1550  
gaatgcttca tagttgtatt ttaattgtat atgtgaaAGA gtcataTTT 1600  
ccaagttata ttTtctaAGA agaAGAAATG atcataAAATC tgacaaggaa 1650  
aaagttgctt acccAAAATC taagtGCTCA atccctgAGC ctcAGCAAAA 1700  
cagctcccCT ccgAGGGAAA tcttataCTT tattGCTCAA ctTTAATTAA 1750  
aatgattgat aataaccACT ttattAAAAA CCTAAGGTTT ttttttttC 1800  
cgtAGACATG ACCACTTTAT taactggTgg tgGGatGCTG ttGTTTctAA 1850  
ttatacctat ttTtcaaggc ttctgttgta ttGAAGTAT catctggTTT 1900  
tgccttaact ctTTAAATTG tatataTTTA tctgtttAGC taatattAA 1950  
ttcaaatacC ccatatctaa atttagtGCA atatcttGTC ttttGtATAG 2000  
gtcataatGAA ttcaTAAAT tatttAtGTC tGTTatAGAA taaAGATTAA 2050  
tatatgttaa aaaaa 2065

<210> 220  
<211> 201  
<212> PRT  
<213> Homo sapiens

<400> 220  
Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu  
1 5 10 15  
Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp  
20 25 30  
Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp  
35 40 45  
Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu  
50 55 60

Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala  
       65                    70                    75  
 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr  
       80                    85                    90  
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe  
       95                    100                   105  
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr  
       110                   115                   120  
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile  
       125                   130                   135  
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe  
       140                   145                   150  
 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val  
       155                   160                   165  
 Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu  
       170                   175                   180  
 Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly  
       185                   190                   195  
 Phe Leu Val Phe Pro Leu  
       200

<210> 221  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 221  
 acggctcacc atgggctccg 20

<210> 222  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 222  
 aggaagagga gcccttggag tccg 24

<210> 223  
 <211> 40

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-40  
<223> Synthetic construct.

<400> 223  
cgtgctggag ggcaagtgtc tggtggtgtg cgactcgaac 40

<210> 224  
<211> 902  
<212> DNA  
<213> Homo sapiens

<400> 224  
cggtggccat gactgcggcc gtgttcttcg gctgcgcctt cattgccttc 50  
gggcctgcgc tcgccttta tgtcttcacc atgcgcatcg agccgttgcg 100  
tatcatcttc ctcatcgccg gagcttcctt ctggtttgtg tctctactga 150  
tttcgtccct tgtttgggtc atggcaagag tcattattga caacaaagat 200  
ggaccaacac agaaatatct gctgatctt ggagcgttg tctctgtcta 250  
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300  
gtgaagggtt gaagagtata aaccagggtg agacagcacc ctctatgcga 350  
ctgctggcct atgtttctgg cttggcttt ggaatcatga gtggagtatt 400  
ttcctttgtg aataccctat ctgactcctt ggggcccaggc acagtggca 450  
ttcatggaga ttctcctcaa ttcttccttt attcagctt catgacgctg 500  
gtcattatct tgctgcatgt attctgggc attgtattt ttgatggctg 550  
tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600  
tggtgtcagc ccagacccatc ataagttctt attatgaaat aaacctggcg 650  
tcagcattta taatcctggt gctcatggc acctggcat tcttagctgc 700  
gggaggcagc tgccgaagcc tgaaaactctg cctgctctgc caagacaaga 750  
actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800  
tcccaaaccg cagactacat ctttagagga agcacaactg tgccttttc 850  
tgaaaatccc ttttctggt ggaattgaga aagaaataaa actatgcaga 900  
ta 902

<210> 225  
<211> 257  
<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly
1				5					10				15	
Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu
				20					25				30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser
				35					40				45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile
				50					55				60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly
				65					70				75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr
				80					85				90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn
				95					100				105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser
				110					115				120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn
				125					130				135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly
				140					145				150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val
				155					160				165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly
				170					175				180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr
				185					190				195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly
				200					205				210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr
				215					220				225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu
				230					235				240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg
				245					250				255	
Ser	Arg													

<210> 226

<211> 3939  
<212> DNA  
<213> Homo sapiens

<400> 226  
cgccaaccag ccgcccac cacccgtgcc actgccccc tgccggggcc 50  
atgttcgctc tgggcttgcc cttcttggtg ctcttggtgg cctcggtcga 100  
gagccatctg ggggttctgg ggcccaagaa cgtctcgacaa aaagacgccc 150  
agttttagcg cacctacgtg gacgaggta acagcgagct ggtcaacatc 200  
tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250  
gtctgtgaac gtcctgaaca agcagaaggg ggccgcgttg ctgtttgtgg 300  
tcccccagaa ggaggctgtg gtgtccttcc aggtgcctt aatcctgcga 350  
gggatgtttc agcgcaagta cctctaccaa aaagtggAAC gaaccctgtg 400  
tcagcccccc accaagaatg agtcggagat tcagttttc tacgtggatg 450  
tgtccaccct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500  
atggacgatt ttgtgctcag gactggggag cagttcagct tcaataccac 550  
agcagcacag ccccaagtact tcaagtatga gttccctgaa ggcgtggact 600  
cggttaattgt caaggtgacc tccaacaagg cttcccttg ctcatc 650  
tccattcagg atgtgctgtg tcctgtctat gacctggaca acaacgttagc 700  
cttcatcgcc atgttaccaga cgatgaccaa gaaggccggcc atcaccgtac 750  
agcgcaaaga cttcccaagc aacagctttt atgtgggtggt ggtggtaag 800  
accgaagacc aagcctgcgg gggctccctg ctttctacc cttcgcaga 850  
agatgaaccg gtcgatcaag ggcacccgcca gaaaaccctg tcagtgcgtgg 900  
tgtctcaagc agtcacgtct gaggcatacg tcagtggat gctctttgc 950  
ctgggtatat ttctctccctt ttacctgctg accgtcctcc tggcctgctg 1000  
ggagaactgg aggcagaaga agaagaccct gctggggcc attgaccgag 1050  
cctgcccaga aagcggtcac cctcgagtcc tggctgattc tttcctggc 1100  
agttccctt atgagggta caactatggc tcctttgaga atgtttctgg 1150  
atctaccgat ggtctggttg acagcgctgg cactggggac ctctcttacg 1200  
gttaccaggc ccgctccctt gaacctgttag gtactccggcc ccgagtgac 1250  
tccatgagct ctgtggagga ggatgactac gacacattga ccgacatcga 1300  
ttccgacaag aatgtcattc gcaccaagca ataccttat gtggctgacc 1350

tggcacggaa ggacaagcgt gttctgcgga aaaagtacca gatctacttc 1400  
tggaacattg ccaccattgc tgtcttctat gcccttcctg tggtgagct 1450  
ggtgatcacc taccagacgg tggtaatgt cacaggaaat caggacatct 1500  
gctactacaa ctccctctgc gcccacccac tgggcaatct cagcgccctc 1550  
aacaacatcc tcagcaacct ggggtacatc ctgctggggc tgctttcct 1600  
gctcatcatc ctgcaacggg agatcaacca caaccgggcc ctgctgcgca 1650  
atgacctctg tgccctgaa tgtggatcc ccaaacactt tgggctttc 1700  
tacgccatgg gcacagccct gatgatggag gggctgctca gtgcggct 1750  
tcatgtgtgc cccaactata ccaatttcca gtttgacaca tcggtcatgt 1800  
acatgatcgc cggaactctgc atgctgaagc tctaccagaa gcggcacccg 1850  
gacatcaacg ccagcgctta cagtgctac gcctgcctgg ccattgtcat 1900  
cttcttctct gtgctggcg tggctttgg caaagggAAC acggcggtct 1950  
ggatcgcttt ctccatcatt cacatcatcg ccaccctgct cctcagcacg 2000  
cagctctatt acatggcccg gtggaaactg gactcggggA tcttccgccc 2050  
catcctccac gtgctctaca cagactgcat ccggcagtgc agcgggccc 2100  
tctacgtgga ccgcatggtg ctgctggta tgggcaacgt catcaactgg 2150  
tcgctggctg cctatggct tatcatgcgc cccaatgatt tcgcttccta 2200  
cttgttggcc attggcatct gcaacctgct ccttacttc gccttctaca 2250  
tcatcatgaa gctccggagt ggggagagga tcaagctcat ccccctgctc 2300  
tgcatcgaaa gcacccctgt ggtctggggc ttgcgcgtct tcttcttctt 2350  
ccagggactc agcacctggc agaaaacccc tgcagagtcg agggagcaca 2400  
accgggactg catcctccctc gacttctttg acgaccacga catctggcac 2450  
ttcctctcct ccatcgccat gttcgggtcc ttcttgggtgt tgctgacact 2500  
ggatgacgac ctggataactg tgcagcggga caagatctat gtcttcttagc 2550  
aggagctggg cccttcgctt cacctcaagg ggccctgagc tcctttgtgt 2600  
catagaccgg tcactctgtc gtgctgtggg gatgagtcgg agcaccgctg 2650  
cccagcactg gatggcagca ggacagccag gtctagcttA ggcttggcct 2700  
gggacagcca tgggggtggca tggAACCTTG cagctgcctt ctgcccggagga 2750  
gcaggcctgc tccccctggaa ccccccagatg ttggccaaat tgctgctttc 2800

ttctcagtgt tggggccttc catgggcccc tgtccttgg ctctccattt 2850  
gtccctttgc aagaggaagg atggaaggga caccctcccc atttcatgcc 2900  
ttgcattttg cccgtcctcc tccccacaat gccccagcct gggacctaag 2950  
gcctctttt cctcccatac tcccactcca gggcctagtc tggggcctga 3000  
atctctgtcc tgtatcaggg ccccagttct ct当地ggctg tccctggctg 3050  
ccatcactgc ccattccagt cagccaggat gnatgggggt atgagatttt 3100  
gggggttggc cagctggtgc cagactttg gtgctaaggc ctgcaagggg 3150  
cctggggcag tgcgtattct ct当地ctctg acctgtgctc agggctggct 3200  
cttagcaat gcgctcagcc caatttggaa accgccttct gattcaagag 3250  
gctgaattca gaggtcacct cttcatccca tcagctccca gactgatgcc 3300  
agcaccagga ctggagggag aagcgccctca ccccttccct tccttcttc 3350  
caggccctta gtcttgccaa accccagctg gtggcccttc agtgcattt 3400  
acactgccc aagaatgtcca gggcaaagg agggatgata cagagttcag 3450  
cccggtctgc ctccacagct gtgggcaccc cagtgctac ctttagaaagg 3500  
ggcttcagga agggatgtgc tgtttccctc tacgtgccca gtcctagcct 3550  
cgctcttagga cccagggctg gcttctaagt ttccgtccag tcttcaggca 3600  
agttctgtgt tagtcatgca cacacatacc tatgaaacct tggagttac 3650  
aaagaattgc cccagctctg ggcacccctgg ccaccctgg ccttggatcc 3700  
ccttcgtccc acctggtcca cccagatgc tgaggatggg ggagctcagg 3750  
cggggcctct gctttggga tggaatgtg ttttctccc aaacttgttt 3800  
ttatagtctc gcttgaaggg ctggagatg aggtgggtct ggatctttc 3850  
tcagagcgtc tccatgctat ggttgcattt ccgtttctta tgaatgaatt 3900  
tgcattcaat aaacaaccag actcaaaaaa aaaaaaaaaa 3939

<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
1					5				10				15	

Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
					20				25				30	



	320	325	330
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala			
335	340	345	
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly			
350	355	360	
Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser			
365	370	375	
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe			
380	385	390	
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val			
395	400	405	
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys			
410	415	420	
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala			
425	430	435	
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe			
440	445	450	
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val			
455	460	465	
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn			
470	475	480	
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly			
485	490	495	
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile			
500	505	510	
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile			
515	520	525	
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu			
530	535	540	
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr			
545	550	555	
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys			
560	565	570	
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met			
575	580	585	
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro			
590	595	600	
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile			
605	610	615	

Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn  
 620 625 630  
 Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr  
 635 640 645  
 Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu  
 650 655 660  
 Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp  
 665 670 675  
 Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val  
 680 685 690  
 Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr  
 695 700 705  
 Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala  
 710 715 720  
 Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile  
 725 730 735  
 Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu  
 740 745 750  
 Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe Phe  
 755 760 765  
 Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu Ser  
 770 775 780  
 Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp  
 785 790 795  
 His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser  
 800 805 810  
 Phe Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln  
 815 820 825  
 Arg Asp Lys Ile Tyr Val Phe  
 830

<210> 228  
 <211> 2848  
 <212> DNA  
 <213> Homo sapiens

<400> 228  
 gctcaagtgc cctgccttgc cccacccagc ccagcctggc cagagcccc 50  
 tggagaagga gctctcttct tgcttggcag ctggaccaag ggagccagtc 100  
 ttgggcgtg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150  
 gctttgtgtc tccgtcccc aggctctccc caaggcccag cctgcagagc 200

tgtctgtgga agttccagaa aactatggtg gaaattccc tttatacctg 250  
accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300  
aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt 350  
ctggcttcct gctggtgacc agggccctgg accgagagga gcaggcagag 400  
taccagctac aggtcacccct ggagatgcag gatggacatg tcttgtgggg 450  
tccacagcct gtgcttgtc acgtgaagga tgagaatgac caggtgcccc 500  
atttctctca agccatctac agagctcgcc tgagccgggg taccaggcct 550  
ggcatccct tcctcttcct tgaggctca gaccggatg agccaggcac 600  
agccaactcg gatcttcgtat tccacatcct gagccaggct ccagcccagc 650  
cttccccaga catgttccag ctggagcctc ggctggggc tctggccctc 700  
agccccaaagg ggagcaccag ctttgaccac gccctggaga ggacctacca 750  
gctgttgta caggtcaagg acatgggtga ccaggcctca ggccaccagg 800  
ccactgccac cgtggaagtc tccatcatag agagcacctg ggtgtcccta 850  
gaggctatcc acctggcaga gaatctaaa gtcctatacc cgaccacat 900  
ggcccaggta cactggagtg ggggtgatgt gcactatcac ctggagagcc 950  
atccccccggg acccttgaa gtgaatgcag agggaaacct ctacgtgacc 1000  
agagagctgg acagagaagc ccaggctgag tacctgctcc aggtgcgggc 1050  
tcagaattcc catggcgagg actatgcggc ccctctggag ctgcacgtgc 1100  
tggtgatgga tgagaatgac aacgtgccta tctgccctcc ccgtgacccc 1150  
acagtcagca tccctgagct cagtcacca ggtactgaag tgactagact 1200  
gtcagcagag gatgcagatg ccccccggctc ccccaattcc cacgttgt 1250  
atcagctcct gagccctgag cctgaggatg gggtagaggg gagagccttc 1300  
caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tcccaactccg 1350  
agcaggccag aacatcctgc ttctggtgct ggccatggac ctggcaggcg 1400  
cagagggtgg cttcagcagc acgtgtgaag tcgaagtgc agtcacagat 1450  
atcaatgatc acgccccctga gttcatcact tcccaagattt ggctataag 1500  
cctccctgag gatgtggagc ccgggactct ggtggccatg ctaacagcca 1550  
ttgatgtgta cctcgagccc gccttccgccc tcatggattt tgccattgag 1600  
aggggagaca cagaaggac tttggcctg gattggagc cagactctgg 1650

gcatgttaga ctcagactct gcaagaacct cagttatgag gcagctccaa 1700  
gtcatgaggt ggtgggttg gtgcagagt tggcgaagct ggtggggcca 1750  
ggcccaggcc ctggagccac cgccacggtg actgtgctag tggagagagt 1800  
gatgccaccc cccaagttgg accaggagag ctacgaggcc agtgtcccc 1850  
tcagtgc(cc) agccggctct ttccctgctga ccatccagcc ctccgacccc 1900  
atcagccgaa ccctcagg(tt) ctccctagtc aatgactcag agggctggct 1950  
ctgcattgag aaattctccg gggaggtgca caccgcccag tccctgcagg 2000  
gcgc(cc)agcc tggggacacc tacacggtgc ttgtggaggc ccaggataca 2050  
gcctgactc ttgcccctgt gcctcccaa tacctctgca caccggcc 2100  
agaccatggc ttgatcgtga gtggacccag caaggacccc gatctggcc 2150  
gtgggcacgg tccctacagc ttccacccctg gtcccaaccc cacggtgcaa 2200  
cgggattggc gcctccagac tctcaatggt toccatgcct acctcacctt 2250  
ggccctgcat tgggtggagc cacgtgaaca cataatcccc gtggtggtca 2300  
gcacacaatgc ccagatgtgg cagctcctgg ttcgagtgtat cgtgtgtcgc 2350  
tgcaacgtgg aggggcagtg catgcgcaag gtgggcccga tgaagggcat 2400  
gc(cc)acgaag ctgtcggcag tgggcacccct tggtaggcacc ctggtagcaa 2450  
taggaatctt cctcatcctc atttcaccc actggaccat gtcaaggaag 2500  
aaggacccgg atcaaccagc agacagcgtg cccctgaagg cgactgtctg 2550  
aatggcccaag gcagctctag ctgggagctt gcctctggc tccatctgag 2600  
tcccctggga gagagccag caccaagat ccagcagggg acaggacaga 2650  
gtagaagccc ctccatctgc cctggggtgg aggcaccatc accatcacca 2700  
ggcatgtctg cagagcctgg acaccaactt tatggactgc ccatggaggt 2750  
gctccaaatg tcagggtgtt tgcccaataa taaagccccaa gagaactggg 2800  
ctgggccta tggaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaag 2848

<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
1				5				10					15	

Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

20	25	30
Glu Asn Tyr Gly Gly	Asn Phe Pro Leu Tyr	Leu Thr Lys Leu Pro
35	40	45
Leu Pro Arg Glu Gly Ala	Glu Gly Gln Ile Val	Leu Ser Gly Asp
50	55	60
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala	Met Asp Pro Asp Ser	
65	70	75
Gly Phe Leu Leu Val Thr Arg Ala	Leu Asp Arg Glu Glu Gln Ala	
80	85	90
Glu Tyr Gln Leu Gln Val Thr Leu Glu Met	Gln Asp Gly His Val	
95	100	105
Leu Trp Gly Pro Gln Pro Val Leu Val	His Val Lys Asp Glu Asn	
110	115	120
Asp Gln Val Pro His Phe Ser Gln Ala	Ile Tyr Arg Ala Arg Leu	
125	130	135
Ser Arg Gly Thr Arg Pro Gly Ile Pro	Phe Leu Phe Leu Glu Ala	
140	145	150
Ser Asp Arg Asp Glu Pro Gly Thr Ala	Asn Ser Asp Leu Arg Phe	
155	160	165
His Ile Leu Ser Gln Ala Pro Ala Gln	Pro Ser Pro Asp Met Phe	
170	175	180
Gln Leu Glu Pro Arg Leu Gly Ala Leu	Ala Leu Ser Pro Lys Gly	
185	190	195
Ser Thr Ser Leu Asp His Ala Leu Glu	Arg Thr Tyr Gln Leu Leu	
200	205	210
Val Gln Val Lys Asp Met Gly Asp Gln	Ala Ser Gly His Gln Ala	
215	220	225
Thr Ala Thr Val Glu Val Ser Ile Ile	Glu Ser Thr Trp Val Ser	
230	235	240
Leu Glu Pro Ile His Leu Ala Glu Asn	Leu Lys Val Leu Tyr Pro	
245	250	255
His His Met Ala Gln Val His Trp Ser	Gly Gly Asp Val His Tyr	
260	265	270
His Leu Glu Ser His Pro Pro Gly Pro	Phe Glu Val Asn Ala Glu	
275	280	285
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp	Arg Glu Ala Gln Ala	
290	295	300
Glu Tyr Leu Leu Gln Val Arg Ala Gln	Asn Ser His Gly Glu Asp	
305	310	315

Tyr Ala Ala Pro Leu Glu Leu His Val Leu Val Met Asp Glu Asn  
                   320                  325                  330  
 Asp Asn Val Pro Ile Cys Pro Pro Arg Asp Pro Thr Val Ser Ile  
                   335                  340                  345  
 Pro Glu Leu Ser Pro Pro Gly Thr Glu Val Thr Arg Leu Ser Ala  
                   350                  355                  360  
 Glu Asp Ala Asp Ala Pro Gly Ser Pro Asn Ser His Val Val Tyr  
                   365                  370                  375  
 Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala  
                   380                  385                  390  
 Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu  
                   395                  400                  405  
 Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met  
                   410                  415                  420  
 Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val  
                   425                  430                  435  
 Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile  
                   440                  445                  450  
 Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro  
                   455                  460                  465  
 Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu  
                   470                  475                  480  
 Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr  
                   485                  490                  495  
 Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val  
                   500                  505                  510  
 Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser  
                   515                  520                  525  
 His Glu Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly  
                   530                  535                  540  
 Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val  
                   545                  550                  555  
 Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu  
                   560                  565                  570  
 Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr  
                   575                  580                  585  
 Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu  
                   590                  595                  600  
 Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly

605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly Asp	
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp	Thr Ala Leu Thr Leu	
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp His	
650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys Asp	Pro Asp Leu Ala Ser	
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly	Pro Asn Pro Thr Val	
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn	Gly Ser His Ala Tyr	
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu	Pro Arg Glu His Ile Ile	
710	715	720
Pro Val Val Val Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val	
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg	
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val	
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile	
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser	Arg Lys Lys Asp Pro Asp	
785	790	795
Gln Pro Ala Asp Ser Val Pro Leu Lys	Ala Thr Val	
800	805	

<210> 230

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 230

cgccttaccg cgcagccgaa agattcacta tggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Seqeunce

<220>  
<221> Artificial Sequence  
<222> full  
<223> Synthetic oligonucleotide probe

<400> 231  
cctgagctgt aaccccaactc cagg 24

<210> 232  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 232  
agagtctgtc ccagctatct tgt 23

<210> 233  
<211> 2786  
<212> DNA  
<213> Homo sapiens

<400> 233  
ccggggacat gaggtggata ctgttcattt gggcccttat tgggtccagc 50  
atctgtggcc aagaaaaatt ttttggggac caagtttga ggattaatgt 100  
cagaaatgga gacgagatca gcaaattttag tcaactatgt aattcaaaca 150  
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200  
gatgtcctgg tcccatctgt cagtctgcag gcatttaaat ctttcctgag 250  
atcccagggc ttagagtgac cagtgacaat tgaggacctg caggcccttt 300  
tagacaatga agatgtatgaa atgcaacaca atgaagggca agaacggagc 350  
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400  
cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450  
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500  
actgggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550  
ttccccagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600  
ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650  
atggatattt tcttgttgc tggccaaat cctgatggat atgtgtatac 700  
tcaaactcaa aaccgattat ggaggaagac gcggtcccgaa aatcctggaa 750  
gctcctgcat tggtgctgac ccaaatacgaa actggaacgc tagtttgca 800  
ggaaaggag ccagcgacaa cccttgctcc gaagtgtacc atggacccca 850

cgccaattcg gaagtggagg tgaaatcagt gtagatttc atccaaaaac 900  
atgggaattt caagggcttc atcgacctgc acagctactc gcagctgctg 950  
atgttatccat atgggtactc agtcaaaaag gccccagatg ccgaggaact 1000  
cgacaagggtg gcgaggcttg cggccaaagc tctggcttct gtgtcgggca 1050  
ctgagttacca agtgggtccc acctgcacca ctgtctatcc agctagcggg 1100  
agcagcatcg actgggcgta tgacaacggc atcaaatttgc cattcacatt 1150  
tgagttgaga gataccggga cctatggctt ctcctgccca gctaaccaga 1200  
tcatccccac tgcagaggag acgtggctgg ggctgaagac catcatggag 1250  
catgtgcggg acaacctcta cttaggcgatg gctctgcctt gtctacattt 1300  
atttgtaccc acacgtgcac gcactgaggc cattgttaaa ggagctcttt 1350  
cctacctgtg tgagtcagag ccctctgggt ttgtggagca cacaggcctg 1400  
ccctctcca gccagctccc tggagtcgtg tgcctggcg gtgtccctgc 1450  
aagaactggt tctgccagcc tgctcaattt tggcctgct gttttgatg 1500  
agcctttgt ctgtttctcc ttccaccctg ctggctgggc ggctgcactc 1550  
agcatcaccc cttcctgggt ggcattgtctc tctctacctc atttttagaa 1600  
ccaaagaaca tctgagatga ttctctaccc tcattcacat ctagccaagc 1650  
cagtgacctt gctctggtgg cactgtggga gacaccactt gtcttaggt 1700  
gggtctcaaa gatgatgttag aatttcctt aatttctcgc agtcttcctg 1750  
gaaaatattt tccttgagc agcaaatctt gtagggatata cagtgaaggt 1800  
ctctccctcc ctccctctctt gttttttttt ttttgagac agagtttgc 1850  
tcttgtgcc caggctggag tgtgatggct cgatcttggc tcaccacaac 1900  
ctctgcctcc tgggttcaag caattctcctt gcctcagcct ctgagtagc 1950  
ttggttata ggccatgcc accatgcctg gctaattttg tgtttttagt 2000  
agagacaggg tttctccatg ttggtcaggc tggctcaaa ctcccaacct 2050  
caggtgatct gccccttgc gcctccaga gtgctggat tacaggtgtg 2100  
agccactgtg ccgggccccgt cccctccctt tttaggcctg aatacaaagt 2150  
agaagatcac ttcccttcac tgtgctgaga atttcttagat actacagttc 2200  
ttactcctctt cttccctttt ttattcagtg tgaccaggat ggccggaggg 2250  
gatctgtgtc actgttaggta ctgtgcccag gaaggctggg tgaagtgacc 2300

atctaaattg caggatggtg aaattatccc catctgtcct aatgggctta 2350  
cctccctttt gcctttgaa ctcacttcaa agatcttaggc ctcatcttac 2400  
aggtcctaaa tcactcatct ggctggata atctcactgc cctggcacat 2450  
tcccatgggt gctgtgggt atccctgtgtt tccttgcct ggtttgtgt 2500  
tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtc 2550  
ttttgtatcc tggaccacaa gttcctaagt agagcaagaa ttcatcaacc 2600  
agctgcctct tgtttcattt cacctcagca cgtaccatct gtcctttgt 2650  
tgttgtgtt ttgttttgt tttttgctt ttaccaaaca tgtctgtaaa 2700  
tcttaacctc ctgccttagga tttgtacagc atctggtgtg tgcttataag 2750  
ccaataaaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile
1														15
Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
					35				40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
					50				55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
					65				70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
					80				85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
					95				100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
					110				115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
					125				130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
					140				145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
					155				160					165

Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile  
 170 175 180  
 His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala  
 185 190 195  
 Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser  
 200 205 210  
 Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro  
 215 220 225  
 Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys  
 230 235 240  
 Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro  
 245 250 255  
 Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp  
 260 265 270  
 Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu  
 275 280 285  
 Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn  
 290 295 300  
 Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met  
 305 310 315  
 Tyr Pro Tyr Gly Tyr Ser Val Lys Ala Pro Asp Ala Glu Glu  
 320 325 330  
 Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val  
 335 340 345  
 Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr  
 350 355 360  
 Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile  
 365 370 375  
 Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly  
 380 385 390  
 Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr  
 395 400 405  
 Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu  
 410 415 420

Tyr

<210> 235  
 <211> 1743  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
caaccatgca aggacagggc aggagaagag gaacctgcaa agacatattt 50  
tgttccaaaa tggcatctta cctttatgga gtactcttg ctgttggcct 100  
ctgtgctcca atctactgtg tgtccccgc caatgcccc agtgcatacc 150  
cccgcccttc ctccacaaag agcacccctg cctcacaggt gtattccctc 200  
aacacccgact ttgccttcg cctataccgc aggctggtt tggagacccc 250  
gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300  
tgctctccct tggggcccac tcagtcacca agacccagat tctccaggc 350  
ctgggcttca acctcacaca cacaccagag tctgccatcc accagggctt 400  
ccagcacctg gttcactcac tgactgtcc cagcaaagac ctgacccctga 450  
agatgggaag tgccctcttc gtcaagaagg agctgcagct gcaggcaa 500  
ttcttggca atgtcaagag gctgtatgaa gcagaagtct tttctacaga 550  
tttctccaac ccctccattt cccaggcgag gatcaacacgc catgtaaaa 600  
agaagaccca agggaaagggtt gtagacataa tccaaggcct tgaccccttg 650  
acggccatgg ttctggtaa tcacatttc tttaaagcca agtgggagaa 700  
gcccttcac cttgaatata caagaaagaa cttcccatcc ctgggtggcg 750  
agcaggtcac tgtgcaagtc cccatgatgc accagaaaga gcagttcgct 800  
tttgggtgg atacagagct gaactgctt gtgctgcaga tggattacaa 850  
gggagatgcc gtggccttct ttgtcctccc tagcaaggc aagatgaggc 900  
aactggaaca ggccttgtca gccagaacac tgataaaagtg gagccactca 950  
ctccagaaaa ggtggataga ggtgttcatc cccagatttt ccatttctgc 1000  
ctcctacaat ctggaaacca tcctccccaa gatgggcattc caaaatgcct 1050  
ttgacaaaaa tgctgattt tctggattt caaagagaga ctccctgcag 1100  
gtttctaaag caacccacaa ggctgtgctg gatgtcagtg aagagggcac 1150  
tgaggccaca gcagctacca ccaccaagtt catagtccga tcgaaggatg 1200  
gtcccttta cttaactgtc tccttcaata ggacccctt gatgtgattt 1250  
acaaataaaag ccacagacgg tattctttt ctagggaaag tggaaaatcc 1300  
cactaaatcc taggtggaa atggcctgtt aactgtatggc acattgctaa 1350  
tgcacaagaa ataacaaacc acatccctct ttctgttctg aggggtgcatt 1400  
tgaccccaagt ggagctggat tcgctggcag ggatgccact tccaaggctc 1450

aatcacaaaa ccatcaacag ggacccaggcacaaggccaa caccattaa 1500  
ccccagtcag tgccctttc cacaattcttcccaggtaac tagttcatg 1550  
ggatgttgct gggttaccat attccatttc ttggggctc ccaggaatgg 1600  
aaatacgcca acccaggta ggcacctcta ttgcagaatt acaataaac 1650  
attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa 1700  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys  
1 5 10 15

Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr  
20 25 30

Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr  
35 40 45

Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val  
50 55 60

Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
65 70 75

Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
80 85 90

Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
95 100 105

Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
110 115 120

Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
125 130 135

Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
140 145 150

Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
155 160 165

Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
170 175 180

Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
185 190 195

Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe		
215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met		
230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn		
245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe		
260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala		
275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys		
290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser		
305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala		
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser		
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser		
350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile		
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn		
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile		
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser		
410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 238  
cttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 239  
tgactcgaaaac cagc 24

<210> 240  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 240  
ggatataggcg gaaggcaaag tcgg 24

<210> 241  
<211> 48  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-48  
<223> Synthetic construct.

<400> 241  
ggcatcttac ctttatggag tactcttgc tttggcctc tgtgctcc 48

<210> 242  
<211> 2436  
<212> DNA  
<213> Homo sapiens

<400> 242  
ggcgaccgt gctacattgc ctggaggaag cctaaggAAC ccaggcatcc 50

agctgcccac gcctgagtcc aagattttc ccaggaacac aaacgttagga 100  
gaccacgct cctggaaagca ccagcctta tcttttacc ttcaagtccc 150  
cttctcaag aatcctctgt tctttgcctt ctaaagtctt ggtacatcta 200  
ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250  
aaaggaaatg ttctccttat gtttgtcta ctattgcatt tagaagctgc 300  
aacaaattcc aatgagacta gcacctctgc caacactgga tccagtgtga 350  
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400  
agtgggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450  
ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500  
gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550  
gccaccaact ctgagtcag cacaacctcc agtggggcca gcacagccac 600  
caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650  
ctgggtccag tgtgacctcc agtggagcca gcactgccac caactctgag 700  
tccagcacag tgtccagtag ggccagcact gccaccaact ctgagtctag 750  
cacactctcc agtggggcca gcacagccac caactctgac tccagcacaa 800  
cctccagtgg ggctagcaca gccaccaact ctgagtcag cacaacctcc 850  
agtggggcca gcacagccac caactctgag tccagcacag tgtccagtag 900  
ggccagcact gccaccaact ctgagtcag cacaacctcc agtggggcca 950  
gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000  
gccaccaact ctgagtcag cacgacacctcc agtggggcca gcacagccac 1050  
caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact 1100  
ctgagtcag cacgacacctcc agtggggcca gcacagccac caactctgag 1150  
tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag 1200  
cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250  
tgtccagtgg gatcagcaca gtcaccaatt ctgagtcag cacaccctcc 1300  
agtggggcca acacagccac caactctgag tccagtacga cctccagtgg 1350  
ggccaacaca gccaccaact ctgagtcag cacagtgtcc agtggggcca 1400  
gcactgccac caactctgag tccagcacaa cctccagtgg ggtcagcaca 1450  
gccaccaact ctgagtcag cacaacctcc agtggggcta gcacagccac 1500

caactctgac tccagcacaa cctccagtga ggccagcaca gccacccaact 1550  
ctgagtctag cacagtgtcc agtggatca gcacagtcac caattctgag 1600  
tccagcacaa cctccagtgg ggccaacaca gccacccaact ctgggtccag 1650  
tgtgacctct gcaggctctg gaacagcgc tctgactgga atgcacacaa 1700  
cttccccatag tgcatctact gcagttagtg aggcaaagcc tgggtgggtcc 1750  
ctgggtccgt gggaaatctt cctcatcacc ctggtctcggtttggcg 1800  
cgtggggctc ttgtgggtcc tcttcttctg tgtgagaaac agcctgtccc 1850  
tgagaaacac cttaacaca gctgtctacc accctcatgg cctaaccat 1900  
ggccttggtc caggccctgg aggaatcat ggagcccccc acaggcccag 1950  
gtggagtcct aactggttct ggaggagacc agtatcatcg atagccatgg 2000  
agatgagcgg gaggaacagc gggccctgag cagccccggaa 2050  
gcattcttca ggaaggaaga gacctggca cccaaacctt ggtttccttt 2100  
cattcatccc aggagacccc tccagcttt gtgtgagatc ctgaaaatct 2150  
tgaagaaggt attcctcacc ttcttgcct ttaccagaca ctggaaagag 2200  
aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250  
acacgacaaa gagaagctgt gctgccccggatctggatctggatctgg 2300  
gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350  
tcaaaatctc cacagtaaaa tccaaagacc taaaaaaaaaaaaaaa 2400  
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
1				5				10					15	
Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
		20						25					30	
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35				40					45	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50				55					60	
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65				70					75	

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	
				80				85				90			
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	
				95				100				105			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				110				115				120			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	
				125				130				135			
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				140				145				150			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				155				160				165			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				170				175				180			
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				185				190				195			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				200				205				210			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				215				220				225			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				230				235				240			
Thr	Asn	Ser	Glu	Ser	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala
				245				250				255			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				260				265				270			
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				275				280				285			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				290				295				300			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				305				310				315			
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	
				320				325				330			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	
				335				340				345			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				350				355				360			
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	

	365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala			
380	385	390	
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala			
395	400	405	
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala			
410	415	420	
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala			
425	430	435	
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val			
440	445	450	
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala			
455	460	465	
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala			
470	475	480	
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala			
485	490	495	
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile			
500	505	510	
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe			
515	520	525	
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn			
530	535	540	
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly			
545	550	555	
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro			
560	565	570	
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile			
575	580	585	
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro			
590	595		

<210> 244  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 244

gaagcaccag ccttatctc ttcacc 26

<210> 245  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic sequence.

<400> 245  
gtcagagttg gtggctgtgc tagc 24

<210> 246  
<211> 48  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-48  
<223> Synthetic construct.

<400> 246  
ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247  
<211> 957  
<212> DNA  
<213> Homo sapiens

<400> 247  
gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcattcc 50  
ttcccgacct tcccagcaat atgcatttgc cacgtctggt cggctcctgc 100  
tccctccttc tgctactggg ggcctgtct ggatggcgcc ccagcgatga 150  
ccccatttag aaggtcatttgc aaggatcaa ccgagggtgc agcaatgcag 200  
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250  
gccggaagg aagtggagaa ggtttcaac ggacttagca acatggggag 300  
ccacacccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350  
tggacaaggat ttccccatgag atcaaccatg gtattggaca agcaggaaag 400  
gaagcagaga agcttggcca tgggtcaac aacgctgctg gacaggccgg 450  
gaaggaagca gacaaagcgg tccaaagggtt ccacactggg gtccaccagg 500  
ctggaaagga agcagagaaa ctggccaag gggtaacca tgctgctgac 550  
caggctggaa aggaagtggaa gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaggagc tgcagaatgc tcataatggg gtcaacccaag 650  
ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750  
agtcaacacg ctttcatca accttccgc cctgtggagg agcgtcgcc 800  
acatcatgcc ctaaaactggc atccggcctt gctggagaa taatgtcgcc 850  
gttgcacat cagctgacat gacctggagg gttgggggt gggggacagg 900  
tttctgaaat ccctgaaggg gttgtactg ggatttgta ataaacttga 950  
tacacca 957

<210> 248  
<211> 247  
<212> PRT  
<213> Homo sapiens

<400> 248  
Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu  
1 5 10 15  
Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu  
20 25 30  
Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg  
35 40 45  
Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His  
50 55 60  
Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met  
65 70 75  
Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu  
80 85 90  
Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile  
95 100 105  
Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn  
110 115 120  
Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln  
125 130 135  
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys  
140 145 150  
Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu  
155 160 165  
Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala  
170 175 180

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
185 190 195  
Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
200 205 210  
Ser Ser His Gln Gly Gly Ala Thr Thr Pro Leu Ala Ser Gly  
215 220 225  
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg  
230 235 240  
Ser Val Ala Asn Ile Met Pro  
245

<210> 249  
<211> 23  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.  
  
<400> 249  
caatatgcatttgcacgtc tgg 23

<210> 250  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 250  
aagcttctct gcttcctttc ctgc 24

<210> 251  
<211> 43  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-43  
<223> Synthetic construct.

<400> 251  
tgacccccatt gagaagggtca ttgaaggat caaccgaggg ctg 43

<210> 252  
<211> 3781  
<212> DNA  
<213> Homo sapiens

<400> 252  
ctccgggtcc ccaggggctg cgccgggccc gcctggcaag ggggacgagt 50  
cagtggacac tccaggaaga gcggccccgc gggggcgat gaccgtgcgc 100  
tgaccctgac tcactccagg tccggaggcg ggggcccccg gggcgactcg 150  
ggggcggacc gcggggcgga gctgccgccc gtgagtcgg ccgagccacc 200  
tgagcccgag cgcgggaca ccgtcgctcc tgctctccga atgctgcga 250  
ccgcgatggg cctgaggagc tggctcgccg cccatgggg cgcgctgccc 300  
cctcgccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350  
gccgcctccg acctgggcgc tcagcccccg gatcagcctg cctctggct 400  
ctgaagagcg gccattcctc agattcgaag ctgaacacat ctccaactac 450  
acagcccttc tgctgagcag ggatggcagg accctgtacg tggtgctcg 500  
agaggccctc tttgcactca gtagcaacct cagttcctg ccaggcgggg 550  
agtaccagga gctgcttgg ggtgcagacg cagagaagaa acagcagtgc 600  
agcttcaagg gcaaggaccc acagcgcgac tgtcaaact acatcaagat 650  
cctcctgccc ctcagcggca gtcacctgtt cacctgtggc acagcagcct 700  
tcagccccat gtgtacctac atcaacatgg agaacttcac cctggcaagg 750  
gacgagaagg ggaatgtcct cctggaagat ggcaagggcc gttgtccctt 800  
cgaccgaat ttcaagtcca ctgccctggt ggttgatggc gagctctaca 850  
ctggaacagt cagcagcttc caaggaaatg acccggccat ctcgcggagc 900  
caaagccttc gccccaccaa gaccgagagc tccctcaact ggctgcaaga 950  
cccagctttt gtggcctcag cctacattcc tgagagcctg ggcagcttgc 1000  
aaggcgatga tgacaagatc tactttttct tcagcgagac tggccaggaa 1050  
tttgagttct ttgagaacac cattgtgtcc cgcattgccc gcatctgcaa 1100  
ggcgatgag ggtggagagc ggtgtctaca gcagcgtgg acctccttcc 1150  
tcaaggccca gctgctgtgc tcacggcccg acgatggctt ccccttcaac 1200  
gtgctgcagg atgtcttcac gctgagcccc agcccccagg actggcgtga 1250  
cacccctttc tatgggtct tcacttccca gtggcacagg ggaactacag 1300  
aaggctctgc cgtctgtgtc ttccacaatga aggatgtca gagagtcttc 1350  
agcggcctct acaaggaggt gaaccgtgag acacagcagt ggtacaccgt 1400  
gaccaccccg gtgcccacac cccggcctgg agcgtgcatac accaacagt 1450

cccgaaaag gaagatcaac tcatccctgc agctcccaga ccgcgtgctg 1500  
aacttcctca aggaccactt cctgatggac gggcagggtcc gaagccgcat 1550  
gctgctgctg cagccccagg ctcgctacca gcgcgtggct gtacaccgcg 1600  
tccctggcct gcaccacacc tacgatgtcc tttcctggg cactggtgac 1650  
ggccggctcc acaaggcagt gagcgtggc ccccggtgc acatcattga 1700  
ggagctgcag atcttctcat cggacagcc cgtcagaat ctgctcctgg 1750  
acacccacag ggggctgctg tatgcggcct cacactcggg cgtagtcag 1800  
gtgccatgg ccaactgcag cctgtaccgg agctgtggg actgcctcct 1850  
cgcccgac ccctactgtg cttggagcgg ctccagctgc aagcacgtca 1900  
gcctctacca gcctcagctg gccaccaggc cgtggatcca ggacatcgag 1950  
ggagccagcg ccaaggacct ttgcagcgcg tttcggttg tgtccccgtc 2000  
tttgtacca acaggggaga agccatgtga gcaagtccag ttccagccca 2050  
acacagtcaa cactttggcc tgcccgctcc tctccaacct ggccacccga 2100  
ctctggctac gcaacggggc ccccgtaat gcctcggcct cctgccacgt 2150  
gctacccact ggggacactgc tgctggtggg caccaacag ctgggggagt 2200  
tccagtgctg gtcactagag gagggcttcc agcagctggt agccagctac 2250  
tgcccgagg tggtgagga cggggtgca gaccaaacag atgagggtgg 2300  
cagtgtaccc gtcattatca gcacatcgcg tgtgagtgc ccagctggtg 2350  
gcaaggccag ctggggtgca gacaggtcct actggaagga gttcctggtg 2400  
atgtgcacgc tctttgtgct ggccgtgctg ctcccagtt tattcttgct 2450  
ctaccggcac cgaaacagca tgaaagtctt cctgaagcag gggaatgtg 2500  
ccagcgtgca ccccaagacc tgccctgtgg tgctgcccc tgagacccgc 2550  
ccactcaacg gccttagggcc ccctagcacc ccgctcgatc accgagggt 2600  
ccagtcctg tcagacagcc ccccgaaaaa ccgagtcctc actgagtcag 2650  
agaagaggcc actcagcatc caagacagct tcgtggaggt atccccagtg 2700  
tgccccggc cccgggtccg cttggctcg gagatccgtg actctgtgg 2750  
gtgagagctg acttccagag gacgctgccc tggcttcagg ggctgtgaat 2800  
gctcgagag ggtcaactgg acctcccctc cgctctgctc ttcgtgaaac 2850  
acgaccgtgg tgcccgcccc ttggagccct tggagccagc tggcctgctg 2900

ctctccagtc aagtagcgaa gctcctacca cccagacacc caaacagccg 2950  
tggccccaga ggtcctggcc aaatatgggg gcctgcctag gttggatggaa 3000  
cagtgccttatgtaaact gagcccttg tttaaaaaac aattccaaat 3050  
gtgaaactag aatgagaggg aagagatgc atggcatgca gcacacacgg 3100  
ctgctccagt tcatggcctc ccaggggtgc tggggatgca tccaaagtgg 3150  
ttgtctgaga cagagttgga aaccctcacc aactggcctc ttcaccttcc 3200  
acattatccc gctgccaccg gctgccctgt ctcaactgcag attcaggacc 3250  
agcttggct gcgtgcgttc tgccttgcca gtcagccgag gatgttagttg 3300  
ttgctgccgt cgccccacca ctcaggac cagaggccta gggtggcact 3350  
gcggccctca ccaggtcctg ggctcgacc caactcctgg acctttccag 3400  
cctgtatcag gctgtggcca cacgagagga cagcgcgagc tcaggagaga 3450  
tttcgtgaca atgtacgcct ttccctcaga attcaggaa gagactgtcg 3500  
cctgccttcc tccgttggcgt cgtgagaacc cgtgtgcccc ttcccaccat 3550  
atccaccctc gctccatctt tgaactaaa cacgaggaac taactgcacc 3600  
ctggtcctct ccccagttccc cagttcaccc tccatccctc accttcctcc 3650  
actctaaggg atatcaaacac tgcccagcac aggggcctg aatttatgtg 3700  
gtttttatac atttttaat aagatgcact ttatgtcatt ttttaataaa 3750  
gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253  
<211> 837  
<212> PRT  
<213> Homo sapiens

<400> 253  
Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro  
1 5 10 15  
Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu  
20 25 30  
Leu Leu Leu Leu Gln Pro Pro Pro Thr Trp Ala Leu Ser  
35 40 45  
Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu  
50 55 60  
Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu  
65 70 75  
Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80	85	90
Phe Ala Leu Ser Ser Asn Leu Ser Phe	Leu Pro Gly Gly Glu	Tyr
95	100	105
Gln Glu Leu Leu Trp Gly Ala Asp Ala	Glu Lys Lys Gln Gln	Cys
110	115	120
Ser Phe Lys Gly Lys Asp Pro Gln Arg	Asp Cys Gln Asn Tyr	Ile
125	130	135
Lys Ile Leu Leu Pro Leu Ser Gly Ser	His Leu Phe Thr Cys	Gly
140	145	150
Thr Ala Ala Phe Ser Pro Met Cys Thr	Tyr Ile Asn Met Glu	Asn
155	160	165
Phe Thr Leu Ala Arg Asp Glu Lys Gly	Asn Val Leu Leu Glu	Asp
170	175	180
Gly Lys Gly Arg Cys Pro Phe Asp Pro	Asn Phe Lys Ser Thr	Ala
185	190	195
Leu Val Val Asp Gly Glu Leu Tyr Thr	Gly Thr Val Ser Ser	Phe
200	205	210
Gln Gly Asn Asp Pro Ala Ile Ser Arg	Ser Gln Ser Leu Arg	Pro
215	220	225
Thr Lys Thr Glu Ser Ser Leu Asn Trp	Leu Gln Asp Pro Ala	Phe
230	235	240
Val Ala Ser Ala Tyr Ile Pro Glu Ser	Leu Gly Ser Leu Gln	Gly
245	250	255
Asp Asp Asp Lys Ile Tyr Phe Phe	Ser Glu Thr Gly Gln	Glu
260	265	270
Phe Glu Phe Phe Glu Asn Thr Ile Val	Ser Arg Ile Ala Arg	Ile
275	280	285
Cys Lys Gly Asp Glu Gly Glu Arg Val	Leu Gln Gln Arg Trp	
290	295	300
Thr Ser Phe Leu Lys Ala Gln Leu Leu	Cys Ser Arg Pro Asp	Asp
305	310	315
Gly Phe Pro Phe Asn Val Leu Gln Asp	Val Phe Thr Leu Ser	Pro
320	325	330
Ser Pro Gln Asp Trp Arg Asp Thr Leu	Phe Tyr Gly Val Phe	Thr
335	340	345
Ser Gln Trp His Arg Gly Thr Thr Glu	Gly Ser Ala Val Cys	Val
350	355	360
Phe Thr Met Lys Asp Val Gln Arg Val	Phe Ser Gly Leu Tyr	Lys
365	370	375

Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro  
380 385 390

Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg  
395 400 405

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu  
410 415 420

Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser  
425 430 435

Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala  
440 445 450

Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe  
455 460 465

Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly  
470 475 480

Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly  
485 490 495

Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu  
500 505 510

Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn  
515 520 525

Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp  
530 535 540

Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu  
545 550 555

Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu  
560 565 570

Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser  
575 580 585

Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln  
590 595 600

Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser  
605 610 615

Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn  
620 625 630

Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu  
635 640 645

Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu  
650 655 660

Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val

665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val Pro	
680	685	690
Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys		
695	700	705
Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val		
710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe		
725	730	735
Leu Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln		
740	745	750
Gly Glu Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu		
755	760	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr		
770	775	780
Pro Leu Asp His Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro		
785	790	795
Gly Ala Arg Val Phe Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile		
800	805	810
Gln Asp Ser Phe Val Glu Val Ser Pro Val Cys Pro Arg Pro Arg		
815	820	825
Val Arg Leu Gly Ser Glu Ile Arg Asp Ser Val Val		
830	835	

<210> 254

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 254

agcccggtgca gaatctgctc ctgg 24

<210> 255

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 255  
tgaagccagg gcagcgctc ctgg 24

<210> 256  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 256  
gtacaggctg cagttggc 18

<210> 257  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-41  
<223> Synthetic construct.

<400> 257  
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 258  
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259  
<211> 4563  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 3635  
<223> unknown base

<400> 259  
ctaagccgga ggatgtgcag ctgcggcgcc ggcgcggct acgaagagga 50  
cggggacagg cgccgtgcga accgagccca gccagccgga ggacgcgggc 100  
agggcgggac gggagccgg actcgtctgc cgccgccgtc gtcgccgtcg 150

tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200  
cgcccagcc gccgctagcg cgcgcgggc atggtcccct cttaaaggcg 250  
caggccgcgg cggcgaaaaa gggtgtgcgg aacaaagcgc cggcgaaaaa 300  
cctgcgggcg gtcgggggc cgcatgggc gcggcgaaa cgcggcgaaa 350  
gcggcgctgc cggggccggg ctcgcggcg cttagggcgaaa ctggcctccg 400  
tgggcggggg cagcgggctg agggcgcgcg gagcctgcgg cggcgaaaaa 450  
ggcgccggcg gcggcccgaa gggcgagcg ggcggggcat ggcgcgcgc 500  
ggccggcgcg cctggctcaag cgtgctgctc gggctcgatc tgggcttcgt 550  
gctggcctcg cggctcgatc tgcccgaaaaa ttccgagctg aagcgagcgg 600  
gcccacggcg cggcgccaa cccgagggt gcgggtccgg gcaggcgaaa 650  
gcttcccagg cggcgaaaaa ggcggcgat ggcgcggggg cgcagctctg 700  
gccggccggc tcggaccagg atggcgcccc gcgcgacagg aactttctct 750  
tcgtggaggt catgaccgccc cagaataacc tgcagactcg ggccgtggcc 800  
gcctacagaa catggtccaa gacaattcct gggaaagttc agttttctc 850  
aagtgggggt tctgacacat ctgtaccaat tccagtagtg ccactacggg 900  
gtgtggacga ctcctacccg ccccagaaga agtccttcat gatgctcaag 950  
tacatgcacg accactactt ggacaagtat gaatggttt tgagagcaga 1000  
tgcgtacgtg tacatcaaag gagaccgtct ggagaacttc ctgaggagtt 1050  
tgaacagcag cgagccctc tttttggcc agacaggctt gggcaccacg 1100  
gaagaaaatgg gaaaactggc cctggagcct ggtgagaact tctgcattgg 1150  
ggggcctggc gtgatcatga gcccggaggt gtttcggaga atggtgcgc 1200  
acattggcaa gtgtctccgg gagatgtaca ccacccatga ggacgtggag 1250  
gtggaaaggt gtgtccggag gtttgcagggt gtgcagtgtg tctggctta 1300  
tgagatgcgg cagttttttt atgagaatta cgagcagaac aaaaagggggt 1350  
acatttagaga tctccataac agtaaaattt accaagctat cacattacac 1400  
cccaacaaaa acccacccta ccagtacagg ctccacagct acatgctgag 1450  
ccgcaagata tccgagctcc gccatcgac aatacagctg caccgcgaaa 1500  
ttgtcctgat gagcaaatac agcaacacag aaattcataa agaggacctc 1550  
cagctggaa tccctccctc cttcatgagg tttcagcccc gccagcgaga 1600

ggagattctg gaatggagt ttctgactgg aaaatacttg tattcggcag 1650  
ttgacggcca gccccctcga agaggaatgg actccgccc gagggaaagcc 1700  
ttggacgaca ttgtcatgca ggtcatggag atgatcaatg ccaacgccaa 1750  
gaccagaggg cgcatcattg acttcaaaga gatccagtag ggctaccgcc 1800  
gggtgaaccc catgtatggg gctgagtagca tcctggacct gctgcttctg 1850  
tacaaaaagc acaaaggaa gaaaatgacg gtccctgtga ggaggcacgc 1900  
gtatttacag cagacttca gcaaaatcca gtttgtggag catgaggagc 1950  
tggatgcaca agagttggcc aagagaatca atcaggaatc tggatccttg 2000  
tccttctct caaactccct gaagaagctc gtcccccttc agctccctgg 2050  
gtcgaagagt gagcacaag aacccaaaga taaaaagata aacatactga 2100  
ttccttgtc tggcggttc gacatgtttg tgagatttat gggaaacttt 2150  
gagaagacgt gtcttatccc caatcagaac gtcaagctcg tggttctgct 2200  
tttcaattct gactccaacc ctgacaaggc caaacaagtt gaactgatga 2250  
gagattaccg cattaagtagc cctaaagccg acatgcagat tttgcctgtg 2300  
tctggagagt tttcaagagc cctggccctg gaagtaggat cctcccagtt 2350  
taacaatgaa tctttgctct tcttctgcga cgtcgacctc gtgtttacta 2400  
cagaattcct tcagcgatgt cgagcaaata cagttctggg ccaacaaata 2450  
tattttccaa tcatcttcag ccagtatgac ccaaagattt tttatagtgg 2500  
gaaagttccc agtgacaacc attttgcctt tactcagaaa actggcttct 2550  
ggagaaaacta tgggttggc atcacgtgt tttataaggg agatcttgc 2600  
cgagtgggtg gctttgatgt ttccatccaa ggctggggc tggaggatgt 2650  
ggacctttc aacaaggttg tccaggcagg tttgaagacg ttttaggagcc 2700  
aggaagtagg agtagtccac gtccaccatc ctgtctttt tgatcccaat 2750  
cttgaccctt aacagtacaa aatgtgctt gggccaaag catcgaccta 2800  
tgggtccacc cagcagctgg ctgagatgtg gctggaaaaa aatgatccaa 2850  
gttacagtaa aagcagcaat aataatggct cagtgaggac agcctaattgt 2900  
ccagcttgc tggaaaagac gtttttaatt atctaattta ttttcaaaa 2950  
atttttgtt ttagttagttt ttgaagtccg tatacaagga tatattttac 3000  
aagtggttt cttacatagg actcccttaa gattgagctt tctgaacaag 3050



attcctgttt tagctgaaga attgttattac atttgagag taaaaaaactt 4550  
aaacacgaaa aaa 4563

<210> 260  
<211> 802  
<212> PRT  
<213> Homo sapiens

<400> 260  
Met Ala Ala Arg Gly Arg Arg Ala Trp Leu Ser Val Leu Leu Gly  
1 5 10 15  
Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg  
20 25 30  
Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro  
35 40 45  
Glu Gly Cys Arg Ser Gly Gln Ala Ala Ser Gln Ala Gly Gly  
50 55 60  
Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser  
65 70 75  
Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly  
80 85 90  
Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala  
95 100 105  
Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe  
110 115 120  
Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro  
125 130 135  
Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe  
140 145 150  
Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu  
155 160 165  
Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg  
170 175 180  
Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe  
185 190 195  
Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu  
200 205 210  
Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val  
215 220 225  
Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly  
230 235 240

Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val  
245 250 255

Gly Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser  
260 265 270

Tyr Glu Met Arg Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys  
275 280 285

Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala  
290 295 300

Ile Thr Leu His Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu  
305 310 315

His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg  
320 325 330

Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser  
335 340 345

Asn Thr Glu Ile His Lys Glu Asp Leu Gln Leu Gly Ile Pro Pro  
350 355 360

Ser Phe Met Arg Phe Gln Pro Arg Gln Arg Glu Glu Ile Leu Glu  
365 370 375

Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr Ser Ala Val Asp Gly  
380 385 390

Gln Pro Pro Arg Arg Gly Met Asp Ser Ala Gln Arg Glu Ala Leu  
395 400 405

Asp Asp Ile Val Met Gln Val Met Glu Met Ile Asn Ala Asn Ala  
410 415 420

Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile Gln Tyr Gly  
425 430 435

Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile Leu Asp  
440 445 450

Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr Val  
455 460 465

Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile  
470 475 480

Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys  
485 490 495

Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser  
500 505 510

Leu Lys Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu  
515 520 525

His Lys Glu Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu

	530	535	540
Ser Gly Arg Phe Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu			
545	550	555	
Lys Thr Cys Leu Ile Pro Asn Gln Asn Val Lys Leu Val Val Leu			
560	565	570	
Leu Phe Asn Ser Asp Ser Asn Pro Asp Lys Ala Lys Gln Val Glu			
575	580	585	
Leu Met Arg Asp Tyr Arg Ile Lys Tyr Pro Lys Ala Asp Met Gln			
590	595	600	
Ile Leu Pro Val Ser Gly Glu Phe Ser Arg Ala Leu Ala Leu Glu			
605	610	615	
Val Gly Ser Ser Gln Phe Asn Asn Glu Ser Leu Leu Phe Phe Cys			
620	625	630	
Asp Val Asp Leu Val Phe Thr Thr Glu Phe Leu Gln Arg Cys Arg			
635	640	645	
Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe Pro Ile Ile Phe			
650	655	660	
Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys Val Pro Ser			
665	670	675	
Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp Arg Asn			
680	685	690	
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val Arg			
695	700	705	
Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp			
710	715	720	
Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe			
725	730	735	
Arg Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe			
740	745	750	
Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly			
755	760	765	
Ser Lys Ala Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met			
770	775	780	
Trp Leu Glu Lys Asn Asp Pro Ser Tyr Ser Lys Ser Ser Asn Asn			
785	790	795	
Asn Gly Ser Val Arg Thr Ala			
800			

<210> 261  
<211> 24

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 261  
gtgccactac ggggtgtgga cgac 24

<210> 262  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 262  
tcccatttct tccgtggtgc ccag 24

<210> 263  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 263  
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264  
<211> 1419  
<212> DNA  
<213> Homo sapiens

<400> 264  
ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactccgc 50  
tgacacccttc ctttcggcc ttgaggttcc cagcctggtg gcccccaggac 100  
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150  
tccttctagt tgcgcttttgc atggcctt cgtctgtgcc ggcttatccg 200  
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250  
agtttttagag aaccttagtac gaagtgttcc ctctggggag ccaggtcgtg 300  
agaaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggaa 350  
tcaaaaattta aggagctagt tacacatgga gacgctcaa ctgagaatga 400

tgtttaacc aatcctatca gtgaagaaac tacaacttgc cctacaggag 450  
gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccccatc 500  
tggtcgatca aaccaaacaa tgttccatt gtttgcatt cagaggaacc 550  
ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600  
aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650  
ccatatgtta cctcatacaa gtcacctgtc accacttag ataagagcac 700  
tggcattgag atctctacag aatcagaaga tgttcctcag ctctcaggtg 750  
aaactgcgt agaaaaaccc gaagagttt gaaagcaccc agagagttgg 800  
aataatgatg acatttgaa aaaaatttta gatattaatt cacaagtgc 850  
acaggcactt cttagtgaca ccagcaaccc agcatataga gaagatattt 900  
aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950  
gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000  
aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgt 1050  
attctagatc taaactctat gaatatttag atattaaatg tgccacca 1100  
gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150  
tagatcaagg agagtcacag ctttattaaa agtttattaa acaataat 1200  
aaaaatttta aacctacttgc atattccata acaaagctga tttaagcaaa 1250  
ctgcatttt tcacaggaga aataatcata ttctgttgc caaaagttgt 1300  
ataaaaatat ttcttatgtt agttcaatgc tgccacatc ttatgtgtc 1350  
atgtgttatg aacaattttc atatgcacta aaaacctaattt taaaataaaa 1400  
atttggttc aggaaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
1				5					10				15	

Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20				25					30	

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
					35			40					45	

Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser

50	55	60
Pro Lys His Val Tyr Ser Ile Ala Ser	Lys Gly Ser Lys Phe Lys	
65	70	75
Glu Leu Val Thr His Gly Asp Ala Ser	Thr Glu Asn Asp Val Leu	
80	85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr	Thr Phe Pro Thr Gly Gly	
95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys His	Thr Glu Ser Thr Pro	
110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val	Ser Ile Val Leu His Ala	
125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu	Pro Glu Pro Glu Pro Glu	
140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro	Arg Met Leu Pro Val Val	
155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val	Thr Ser Tyr Lys Ser Pro	
170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly	Ile Glu Ile Ser Thr Glu	
185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly	Glu Thr Ala Ile Glu Lys	
200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu	Ser Trp Asn Asn Asp Asp	
215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn	Ser Gln Val Gln Gln Ala	
230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala	Tyr Arg Glu Asp Ile Glu	
245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser	Leu Ala Leu Ala Ala Ala	
260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr	Lys Ser Gln Leu Leu Pro	
275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp	Asp Ile Glu Thr Val Ile	
290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys	Leu Tyr Glu Tyr Leu Asp	
305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg	Glu Lys Ala Ala Thr Val	
320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg	Ser Arg Arg Val Thr Ala	
335	340	345

Leu Leu Lys Val Tyr  
350

<210> 266  
<211> 2403  
<212> DNA  
<213> Homo sapiens

<400> 266  
cggttcgagc ggctcgagt aagaggctct ccacggctcc tgccgcctgag 50  
acagctggcc tgacctccaa atcatccatc cacccctgct gtcatctgtt 100  
ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150  
tttggttctc agtttctacg agctgggtgc aggacagtgg caagtcactg 200  
gaccgggcaa gtttgcacag gccttggtgg gggaggacgc cgtgttctcc 250  
tgctccctct ttcctgagac cagtcacagag gctatggaag tgccgttctt 300  
cagaatcag ttccatgctg tggcacct ctacagagat gggaaagact 350  
ggaaatctaa gcagatgcc a cgtatcgag ggagaactga gtttgtgaag 400  
gactccattt caggggggcg tgtctctcta aggctaaaaa acatcactcc 450  
ctcggacatc ggcctgtatg ggtgtggtt cagttccac atttacgatg 500  
aggaggccac ctgggagctg cgggtggcag cactgggctc acttcctctc 550  
atttccatcg tggatatgt tgacggaggt atccagttac tctgcctgtc 600  
ctcaggctgg ttcccccagc ccacagccaa gtggaaaggt ccacaaggac 650  
aggatttgc ttcagactcc agagcaaatg cagatggta cagcctgtat 700  
gatgtggaga tctccattat agtccaggaa aatgctggta gcatattgt 750  
ttccatccac cttgctgagc agagtcatga ggtgaaatcc aaggatttga 800  
taggagagac gttttccag ccctcacctt ggccgcctggc ttctattta 850  
ctcggttac tctgtggtgc cctgtgtggt gttgtcatgg ggtatgataat 900  
tgtttcttc aaatccaaag gaaaatcca ggcggaaactg gactggagaa 950  
gaaaggcacgg acaggcagaa ttgagagacg cccggaaaca cgcagtggag 1000  
gtgactctgg atccagagac ggctcacccg aagctctgcg tttctgtatct 1050  
gaaaactgtt acccatagaa aagctccccca ggaggtgcct cactctgaga 1100  
agagattttac aaggaagagt gtgggtggctt ctcagggttt ccaagcaggg 1150  
agacattact gggaggtgga cgtgggacaa aatgttaggtt ggtatgtggg 1200  
agtgtgtcg gatgacgttag acaggggaa gaacaatgtg actttgtctc 1250

ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtattc 1300  
acattcaatc cccatTTTat cagcctcccc cccagcaccc ctcc tacacg 1350  
agttaggggtc ttccctggact atgagggtgg gaccatctcc ttcttcaata 1400  
caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450  
tttgtgagac cctatatcca gcatgcgatg tatgacgagg aaaaggggac 1500  
tcccattttc atatgtccag tgtcctgggg atgagacaga gaagaccctg 1550  
cttaaaggc cccacaccac agacccagac acagccaagg gagagtgctc 1600  
ccgacaggtg gccccagctt cctctccgga gcctgcgcac agagagtcac 1650  
gccccccact ctccctttagg gagctgaggt tcttctgccc tgagccctgc 1700  
agcagcggca gtcacagctt ccagatgagg ggggattggc ctgaccctgt 1750  
gggagtcaga agccatggct gccctgaagt ggggacggaa tagactcaca 1800  
ttaggttag tttgtaaaaa ctccatccag ctaagcgatc ttgaacaagt 1850  
cacaacctcc caggctccctc atttgcttagt cacggacagt gattcctgcc 1900  
tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcaggtt 1950  
tgagggcaca gtgttgcta atgatgtgtt tttatattat acattttccc 2000  
accataaact ctgtttgctt attccacatt aatttacttt tctctataacc 2050  
aaatcaccctt tggaaatagtt attgaacacc tgctttgtga ggctcaaaga 2100  
ataaaagagga ggtaggattt ttcaactgatt ctataagccc agcattacct 2150  
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200  
gtccatatcc ctcatTAACA cagacacaaa aattctaaat aaaattttaa 2250  
caaattaaac taaacaatAT atttaaagat gatataaac tactcagtgt 2300  
ggtttgcctt acaaatgcag agttggttt aatTTAAAT atcaaccagt 2350  
gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400  
aaa 2403

<210> 267  
<211> 466  
<212> PRT  
<213> Homo sapiens

<400> 267  
Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val  
1 5 10 15  
Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

20	25	30
Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu		
35	40	45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe		
50	55	60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser		
65	70	75
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp		
80	85	90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr		
95	100	105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile		
110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly		
125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile		
140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala		
155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg		
170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile		
185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu		
200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu		
215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu		
230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile		
245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp		
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys		
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys		
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro		
305	310	315

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
320									325					330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val
335									340					345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp
350									355					360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn
365									370					375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr
380									385					390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr
395									400					405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe
410									415					420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys
425									430					435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr
440									445					450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp
455									460					465

Gly

<210> 268  
<211> 2103  
<212> DNA  
<213> Homo sapiens

<400> 268  
ccttcacagg actcttcatt gctgggtggc aatgatgtat cggccagatg 50  
tggtgagggc taggaaaaga gtttgggg aaccctgggt tatcggcctc 100  
gtcatcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150  
tcatttatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200  
tgtcattttac aactgacaaa ctatatgctg agttggcag agaggcttct 250  
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
attttataaa tctccattaa gggagaatt tgtcaagtct caggttatca 350  
agttcagtca acagaagcat ggagtgttgg ctcataatgct gttgatttgc 400  
agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450  
tgtttacat gaaaagctgc aagatgctgt aggacccct aaagtagatc 500

ctcactcagt taaaataaaa aaaatcaaca agacagaaac agacagctat 550  
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600  
caggatcggtt ggtgggacag aagtagaaga gggtaatgg ccctggcagg 650  
ctagcctgca gtggatggg agtcatcgct gtggagcaac cttattaat 700  
gccacatggc ttgtgagtc tgctcactgt tttacaacat ataagaaccc 750  
tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800  
aacgggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850  
catgactatg atatttcct tgcaagcctt tctagccctg ttccctacac 900  
aaatgcagta catagagttt gtctccctga tgcatcctat gagttcaac 950  
caggtgatgt gatgtttgtg acaggattt gggactgaa aaatgatgg 1000  
tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050  
aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100  
tatgtgctgg ctcccttagaa ggaaaaacag atgcattcca gggtgactct 1150  
ggaggaccac tggtagttc agatgctaga gatatctggt accttgctgg 1200  
aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctgggtttt 1250  
atactagagt tacggccttg cggactgga ttacttcaaa aactggtac 1300  
taagagacaa aagcctcatg gaacagataa cattttttt tgggggggg 1350  
gtgtggaggc catttttaga gatacagaat tggagaagac ttgcaaaaca 1400  
gctagatttgc actgatctca ataaactgtt tgcttgatgc atgtatccc 1450  
ttcccaagctc tgcccgac gtaagcatcc tgcttctgcc agatcaactc 1500  
tgtcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata 1550  
atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt 1600  
cagaattttg acttggac ataaatttgc aatgcataata tacaatttgc 1650  
agcaactcctt ttcttcagtt cctcagctcc tctcatttca gcaaataatcc 1700  
atttcaagg tgcagaacaa ggagtgaaag aaaatataag aaaaaaaaaa 1750  
tccctacat ttattggca cagaaaagta ttaggtgtt ttcttagtgg 1800  
aatatttagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850  
aataccaatc acttcattcat ttaggaagta tggaaactaa gttaaggaag 1900  
tccagaaaga agccaagata ttcatttccaa aacaactact 1950

atgataaaatg tgaagaagat tctgttttt tgtgacctat aataattata 2000  
caaacttcat gcaatgtact tggtaaaggc aaattaaaggc aaatatttat 2050  
ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100  
cca 2103  
  
<210> 269  
<211> 423  
<212> PRT  
<213> Homo sapiens  
  
<400> 269  
Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys  
1 5 10 15  
Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile  
20 25 30  
Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr  
35 40 45  
Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
50 55 60  
Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
65 70 75  
Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
80 85 90  
Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
95 100 105  
Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
110 115 120  
Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
125 130 135  
Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
140 145 150  
Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
155 160 165  
Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
170 175 180  
Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
185 190 195  
Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
200 205 210  
Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr  
215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230				235					240	
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
	245					250					255			
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
	260				265					270				
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
	275					280				285				
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
	290					295			300					
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
	305					310				315				
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
	320					325				330				
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
	335					340				345				
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
	350					355				360				
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
	365					370				375				
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
	380					385				390				
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
	395					400				405				
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
	410					415					420			
Thr	Gly	Ile												

<210> 270  
<211> 1170  
<212> DNA  
<213> Homo sapiens

<400> 270  
gtcgaagggtt ataaaagctt ccagccaaac ggcattgaag ttgaagatac 50  
aacctgacag cacagcctga gatcttgggg atccctcagc ctaacaccca 100  
cagacgtcag ctggtgatt cccgctgcat caaggcctac ccactgtctc 150  
catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200  
ttcccaagac tcagcccttg gccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgccttg ccggctgtcc cctgcgacta 300  
cgaccactgc cgacacctgc aggtgccctg caaggagcta cagagggtcg 350  
ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400  
gaccgcgcgc gcatgggaga agtgcgcatt gcggccgaag agggccgcgc 450  
agtggtccac tggtgtgccc cttctccccc gtcctccac tactggctgc 500  
tgctttggga cggcaggcag gctgcgcaga agggccccc gctgaacgct 550  
acggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600  
cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650  
ctggaggaga gggcctcgag gggccgaca tccctgcctt cggcccttgc 700  
agccgccttg cgggtccgccc caaccccccgc actctggtcc acgcggccgt 750  
cgggtgggc acggccctgg ccctgctaag ctgtgcgcgc ctgggtgtggc 800  
acttctgcct gcgcatcgc tggggctgcc cgcgcgcgc cggcccccga 850  
gccgcagggg cgctctgaaa gggcctggg ggcatctcg gcacagacag 900  
ccccacactgg ggcgctcagc ctggcccccgg gaaagagagga aaacccgctg 950  
cctccaggaa gggctggacg gcgagctggg agccagcccc aggctccagg 1000  
gccacggcgg agtcatggtt ctcaggactg agcgcttgc taggtccgg 1050  
acttggcgct ttgtttcctg gctgaggctc gggaaaggaat agaaaggggc 1100  
ccccaaatttt ttttaagcg gccagataat aaataatgta accttgcgg 1150  
ttaaaaaaaaaaaaaaa 1170

<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

Met	Leu	Gly	Ser	Pro	Cys	Leu	Leu	Trp	Leu	Leu	Ala	Val	Thr	Phe
1														15
Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
														30
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
														45
Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys
														60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly
														75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu
80						85						90		
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys
95							100					105		
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp
110							115					120		
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val
125							130					135		
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val
140							145					150		
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro
155							160					165		
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe
170							175					180		
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu
185							190					195		
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser
200							205					210		
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly
215							220					225		
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu		
230							235							

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

```

agagaaaagaa gcgtctccag ctgaagccaa tgcagccctc cggctctccg 50
cgaagaagtt ccctgccccg atgagccccc gccgtgcgtc cccgactatac 100
cccaggcggg cgtggggcac cgggcccagc gccgacgatc gctgccgttt 150
tgccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgccctgctct 250
acgcctcaa tctgctctt tggtaatgt ccatcagtgt gttggcagtt 300
tctgcttggaa tgagggacta cctaaataat gttctcaatt taactgcaga 350
aacgagggtaa gaggaagcag tcattttgac ttactttcct gtggttcatc 400
cggtcatgtat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450
tattgtggaa cggtgaaaag aaatctgttg cttcttgcatt ggtactttgg 500

```

aagtttgctt gtcattttct gtgtagaact ggcttgccc gtttggacat 550  
atgaacagga acttatggtt ccagtacaat ggtcagatat ggtcactttg 600  
aaagccagga tgacaaatta tggattacct agatatcggt ggcttactca 650  
tgcttggaat tttttcaga gagagttaa gtgctgtgga gtagtatatt 700  
tcactgactg gttggaaatg acagagatgg actggcccc agattcctgc 750  
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800  
cagtgacctt tatcaagagg gttgtggaa gaaaatgtat tccttttga 850  
gaggaaccaa acaactgcag gtgctgaggt ttctggaat ctccattggg 900  
gtgacacaaa tcctggccat gattctcacc attactctgc tctggctct 950  
gtattatgat agaagggagc ctgggacaga ccaaattgatg tccttgaaga 1000  
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050  
agcctgtcaa gaatcttga acacacatcc atggcaaaca gcttaatac 1100  
acacttttag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150  
caaacttggtt ttattggact tgtgaatttt tgagtacata ctatgtgtt 1200  
cagaaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250  
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300  
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350  
acccactgtg tagcctgtgt atgactttta ctgaacacag ttatgtttg 1400  
aggcagcatg gtttgattag cattccgca tccatgcaaa cgagtcacat 1450  
atggtggac tggagccata gtaaaggttg atttacttct accaactagt 1500  
atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata 1550  
acttttatta ctcagcgatc tattttctg atgctaaata aattatata 1600  
cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctggta 1650  
ctaaaatatt cttaccactt aaaagagcaa gctaacacat tgtcttaagc 1700  
tgatcaggga tttttgtat ataagtctgt gttaaatctg tataattcag 1750  
tcgatttcag ttctgataat gtttggaaaata accattatga aaaggaaaat 1800  
ttgtcctgta tagcatcatt atttttagcc tttcctgtta ataaagctt 1850  
actattctgt cctggcctta tattacacat ataactgttta tttaaataact 1900  
taaccactaa ttttggaaaat taccagtgtg atacatagga atcattattc 1950

agaatgtagt ctggccttta ggaagtatta ataagaaaat ttgcacataa 2000  
cttagttgat tcagaaagga cttgtatgct gttttctcc caaatgaaga 2050  
ctcttttga cactaaacac tttttaaaaa gcttatctt gccttcctca 2100  
aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg 2150  
ttcttttct ccagaaaaat gcttgatgaga atcattaaaa catgtgacaa 2200  
tttagagatt cttgtttta tttcactgat taatatactg tggcaaatta 2250  
cacagattat taaattttt tacaagagta tagtataattt attgaaatg 2300  
ggaaaagtgc attttactgt attttgtgta ttttgttat ttctcagaat 2350  
atgaaaagaa aattaaaatg tgtcaataaa tattttctag agagtaa 2397

<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

Met	Ala	Arg	Glu	Asp	Ser	Val	Lys	Cys	Leu	Arg	Cys	Leu	Leu	Tyr
1				5					10					15
Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20				25						30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35				40						45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50				55						60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65				70						75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80				85						90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95				100						105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110				115						120
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
				125				130						135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
				140				145						150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
				155				160						165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser

170	175	180
Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln		
185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met		
200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe		
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu		
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro		
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His		
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg		
275	280	285
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe		
290	295	300
Glu Met Glu Glu Leu		
305		
<210> 274		
<211> 2063		
<212> DNA		
<213> Homo sapiens		
<400> 274		
gagagaggca gcagcttgct cagcggacaa ggatgctggg cgtgaggcac 50		
caaggcctgc cctgcactcg ggccctctcc agccagtgct gaccaggcac 100		
ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctccctgctgc 150		
cttggggta caatctcagc tccaggctac agggagaccc ggaggatcac 200		
agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct 250		
cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300		
aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350		
attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400		
cgggcagcct ctccacttca tcccggagaa gcagctgtgt gacggagagc 450		
tggactgtcc cttggggag gacgaggagc actgtgtcaa gagcttcccc 500		
gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550		
ggtgctggac tcggccacag ggaactggtt ctctgcctgt ttcgacaact 600		

tcacagaagc tctcgctgag acagcctgta ggcagatggg ctacagcaga 650  
gctgtggaga ttggccaga ccaggatctg gatgttggaa aatcacaga 700  
aaacagccag gagcttcgca tgccgaactc aagtggccc tgtctctcag 750  
gctccctggc ctccctgcac tgtcttgccct gtggaaagag cctgaagacc 800  
ccccgtgtgg tgggtgggaa ggaggcctct gtggattctt ggccttggca 850  
ggtcagcatc cagtagcaca aacagcacgt ctgtggaggg agcatcctgg 900  
accccccactg ggtcctcactg gcagcccact gttcaggaa acataccgat 950  
gtgttcaact ggaagggtgcg ggcaggctca gacaaactgg gcagcttccc 1000  
atccctggct gtggccaaga tcatacatcat tgaattcaac cccatgtacc 1050  
ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcaacttc 1100  
tcagggcacag tcagggccat ctgtctgccc ttcttgatg aggagctcac 1150  
tccagccacc ccactctgga tcattggatg gggcttacg aagcagaatg 1200  
gagggaaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250  
agcacacggc gcaatgcaga cgatgcgtac cagggggaa tcaccgagaa 1300  
gatgatgtgt gcaggcatcc cgaaaggggg tgtggacacc tgccagggtg 1350  
acagtggtgg gcccctgatg taccaatctg accagtgca tgtggggc 1400  
atcgtagct gggctatgg ctgcggggc ccgagcaccc caggagtata 1450  
caccaaggc tcagcctatc tcaactggat ctacaatgtc tggaggctg 1500  
agctgtaatg ctgctgcccc tttgcagtgc tggagccgc ttcccttcctg 1550  
ccctgcccac ctggggatcc cccaaagtca gacacagagc aagagtcccc 1600  
ttgggtacac ccctctgccc acagcctcag catttcttgg agcagcaaag 1650  
ggcctaatt cctgttaagag accctcgca cccagaggcg cccagaggaa 1700  
gtcagcagcc ctagctcgcc cacacttggt gctcccagca tcccaggag 1750  
agacacagcc cactgaacaa ggtctcaggg gtattgttaa gccaaagg 1800  
aactttccca cactactgaa tggaaagcagg ctgtcttgta aaagcccaga 1850  
tcactgtggg ctggagagga gaaggaaagg gtctgcgccca gcccgtccg 1900  
tcttcaccca tccccaaagcc tactagagca agaaaccagt tgtaatataa 1950  
aatgcactgc cctactgttg gtatgactac cgttacccac tgggttcatt 2000  
gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050

caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp  
1 5 10 15

Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg  
20 25 30

Lys Val Gly Ile Pro Ile Ile Ala Leu Leu Ser Leu Ala Ser  
35 40 45

Ile Ile Ile Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr  
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln  
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu  
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg  
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr  
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu  
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu  
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn  
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser  
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu  
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Ala Ser Val Asp Ser  
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys  
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His  
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala  
245 250 255

Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys
			260						265					270
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp
				275					280					285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr
				290					295					300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Asp	Glu	Glu	Leu	Thr	Pro	
				305				310					315	
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn
				320				325					330	
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val
				335				340					345	
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu
				350				355					360	
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val
				365				370					375	
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser
				380				385					390	
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys
				395				400					405	
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr
				410				415					420	
Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu			
				425				430						
<210>	276													
<211>	3143													
<212>	DNA													
<213>	Homo sapiens													
<400>	276													
gggctgaggc	actgagagac	cggaaaggct	ggcattccag	agggagggaa	50									
acgcagcggc	atccccaggc	tccagagctc	cctggtgaca	gtctgtggct	100									
gagcatggcc	ctcccagccc	tggcctgga	cccctggagc	ctcctgggcc	150									
ttttcctctt	ccaactgctt	cagctgctgc	tgccgacgac	gaccgcgggg	200									
ggaggcgggc	aggggcccatt	gcccagggtc	agatactatg	cagggatga	250									
acgttagggca	cttagcttct	tccaccagaa	gggcctccag	gattttgaca	300									
ctctgctcct	gagtggtgat	ggaaatactc	tctacgtggg	ggctcgagaa	350									
gccattctgg	ccttggatat	ccagggatcca	ggggtccccca	ggctaaagaa	400									

catgataccg tggccagcca gtgacagaaa aaagagtcaa tgtgcctta 450  
agaagaagag caatgagaca cagtgttca acttcattcg tgtcctggtt 500  
tcttacaatg tcacccatct ctacacctgc ggcaccccg cttcagccc 550  
tgcttgtacc ttcatgttac ttcaagattc ctacctgttgc cccatctcg 600  
aggacaaggt catggagggaa aaaggccaaa gccccttga ccccgctcac 650  
aagcatacgg ctgtcttgggt ggatgggatg ctctattctg gtactatgaa 700  
caacttcctg ggcagtgagc ccatcctgat ggcacactg ggatcccagc 750  
ctgtcctcaa gaccgacaac ttccctccgtt ggctgcatca tgacgcctcc 800  
tttgtggcag ccattcccttc gacccaggc gtctacttct tcttcgagga 850  
gacagccagc gagtttgact tctttgagag gctccacaca tcgcgggtgg 900  
ctagagtctg caagaatgac gtgggcggcg aaaagctgct gcagaagaag 950  
tggaccacct tcctgaaggc ccagctgctc tgccacccagc cggggcagct 1000  
gcccttcaac gtcatccgccc acgcggctt gctccccggc gattctccca 1050  
cagctccccca catctacgca gtcttccacctt cccagtgca ggttggcggg 1100  
accaggagct ctgcggtttg tgccttctt ctcttggaca ttgaacgtgt 1150  
ctttaagggg aaatacaaag agttgaacaa agaaacttca cgctggacta 1200  
cttatagggg ccctgagacc aaccccccggc caggcagttt ctcagtgggc 1250  
ccctccctcg ataaggccct gacccatcg aaggaccatt tcctgatgga 1300  
tgagcaagtg gtggggacgc ccctgctgggt gaaatctggc gtggagtata 1350  
cacggcttgc agtggagaca gcccaggggcc ttgatggca cagccatctt 1400  
gtcatgttacc tgggaaccac cacagggtcg ctccacaagg ctgtggtaag 1450  
tggggacagc agtgcgtatc tggtaaga gattcagctg ttccctgacc 1500  
ctgaacctgt tcgcaacctg cagctggccc ccacccaggc tgcaagtgtt 1550  
gtaggcttct caggagggtgt ctggagggtg ccccgagcca actgttagtgt 1600  
ctatgagagc tgggtggact gtgtccttgc cggggacccc cactgtgcct 1650  
gggaccctga gtcccgaaacc tggccctcc tgtctgcccc caacctgaac 1700  
tcctggaaagc aggacatgga gggggggaaac ccagagtggg catgtgccag 1750  
tggccccatg agcaggagcc ttccggcctca gagccgcccc caaatcatta 1800  
aagaagtccct ggctgtcccc aactccatcc tggagctcccc ctgcccccac 1850

ctgtcagcct tggccttta ttattggagt catggccag cagcagtccc 1900  
agaaggctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950  
atggagttgg gggctctac cagtgctggg caactgagaa tggctttca 2000  
taccctgtga tctcctactg ggtggacagc caggaccaga ccctggccct 2050  
ggatcctgaa ctggcaggca tccccggga gcatgtgaag gtcccgttga 2100  
ccagggtcag tggtggggcc gccctggctg cccagcagtc ctactggccc 2150  
cactttgtca ctgtcactgt cctcttgcc ttagtgctt caggagccct 2200  
catcatcctc gtggcctccc cattgagago actccggct cggggcaagg 2250  
ttcagggctg tgagaccctg cgccctgggg agaaggcccc gttaagcaga 2300  
gagcaacacc tccagtctcc caaggaatgc aggacctctg ccagtgtatgt 2350  
ggacgctgac aacaactgcc taggcactga ggtagctaa actctaggca 2400  
cagggccgggg ctgcggtgca ggcacctggc catgctggct gggcgcccc 2450  
agcacagccc tgacttaggat gacagcagca caaaagacca ctttctccc 2500  
ctgagaggag cttctgtac tctgcatcac ttagtgcact cagcagggtg 2550  
atgcacagca gtctgcctcc cctatggac tcccttctac caagcacatg 2600  
agctctctaa cagggtgggg gctaccccca gacctgctcc tacactgata 2650  
ttgaagaacc tggagaggat cttcagttc tggccattcc agggaccctc 2700  
cagaaacaca gtgttcaag agaccctaaa aaacctgcct gtcccaggac 2750  
cctatggtaa tgaacaccaa acatctaaac aatcatatgc taacatgcc 2800  
ctcctggaaa ctccactctg aagctgccgc tttggacacc aacactccct 2850  
tctcccaggg tcatgcaggg atctgctccc tcctgcttcc cttaccagtc 2900  
gtgcaccgct gactcccagg aagtcttcc tgaagtctga ccaccttct 2950  
tcttgcttca gttggggcag actctgatcc cttctgccc ggcagaatgg 3000  
caggggtaat ctgagccttc ttcaactcatt taccctagct gacccttca 3050  
cctctccccc tccctttcc tttgtttgg gattcagaaa actgcttgtc 3100  
agagactgtt tatttttat taaaaatata aggctaaaaa aaa 3143

<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly  
 1 5 10 15

Leu Phe Leu Phe Gln Leu Leu Gln Leu Leu Leu Pro Thr Thr Thr  
 20 25 30

Ala Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr  
 35 40 45

Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly  
 50 55 60

Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr  
 65 70 75

Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln  
 80 85 90

Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala  
 95 100 105

Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn  
 110 115 120

Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn  
 125 130 135

Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala  
 140 145 150

Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser  
 155 160 165

Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro  
 170 175 180

Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser  
 185 190 195

Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg  
 200 205 210

Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg  
 215 220 225

Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr  
 230 235 240

Gln Val Val Tyr Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp  
 245 250 255

Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys  
 260 265 270

Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr  
 275 280 285

Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro

	290	295	300
Phe Asn Val Ile Arg His Ala Val Leu	Leu Pro Ala Asp Ser	Pro	
305	310	315	
Thr Ala Pro His Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln	Val	
320	325	330	
Gly Gly Thr Arg Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp		
335	340	345	
Ile Glu Arg Val Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys	Glu	
350	355	360	
Thr Ser Arg Trp Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro	Arg	
365	370	375	
Pro Gly Ser Cys Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu	Thr	
380	385	390	
Phe Met Lys Asp His Phe Leu Met Asp	Glu Gln Val Val Gly	Thr	
395	400	405	
Pro Leu Leu Val Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala	Val	
410	415	420	
Glu Thr Ala Gln Gly Leu Asp Gly His	Ser His Leu Val Met	Tyr	
425	430	435	
Leu Gly Thr Thr Thr Gly Ser Leu His	Lys Ala Val Val Ser	Gly	
440	445	450	
Asp Ser Ser Ala His Leu Val Glu Glu	Ile Gln Leu Phe Pro	Asp	
455	460	465	
Pro Glu Pro Val Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly	Ala	
470	475	480	
Val Phe Val Gly Phe Ser Gly Gly Val	Trp Arg Val Pro Arg	Ala	
485	490	495	
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala	Arg	
500	505	510	
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys	Leu	
515	520	525	
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu	Arg	
530	535	540	
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg	Ser	
545	550	555	
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu	Ala	
560	565	570	
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser	Ala	
575	580	585	

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu  
590 595 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln  
605 610 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly  
620 625 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln  
635 640 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His  
650 655 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala  
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu  
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser  
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu  
710 715 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His  
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp  
740 745 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala  
755 760

<210> 278

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 278

ctgctggta aatctggcgt ggag 24

<210> 279

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 279  
gtctggtcct ggctgtccac ccag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 280  
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281  
<211> 2320  
<212> DNA  
<213> Homo sapiens

<400> 281  
agggtccctt agccgggcgc agggcgcgca gcccaggctg agatccgcgg 50  
cttccgtaga agtgagcatg gctgggcagc gagtgcttct tctagtggc 100  
ttccttctcc ctggggtcct gctctcagag gctgccaaaa tcctgacaat 150  
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
ttcttcaaga tcacggtcat aatgtcacca tgcttaacca caaaagaggt 250  
ccttttatgc cagatttaa aaaggaagaa aaatcatatc aagttatcag 300  
ttggcttgca cctgaagatc atcaaagaga attaaaaag agttttgatt 350  
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400  
aatgttctag aatacttggc gttgcagtgc agtcatttt taaatagaaa 450  
ggatatcatg gattccttaa agaatgagaa cttcgacatg gtgatagttg 500  
aaactttga ctactgtcct ttccctgattt ctgagaagct tggaaagcca 550  
tttgtggcca ttctttccac ttcatcgcc tctttggaat ttgggctacc 600  
aatcccccttg tcttatgttc cagtattccg ttccctgctg actgatcaca 650  
tggacttctg gggccgagtg aagaattttc ttagtgc 700  
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750  
tttcacagaa ggctctaggc cagtttgtc tcattttcta ctgaaagcag 800  
agttgtggtt cattaactct gactttgcct ttgatttgc tcgacacctg 850  
cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

agtaccacaa gacttggaga acttcattgc caagttggg gactctgggt 950  
ttgtccttgt gacccctgggc tccatggta acacacctgtca gaatccggaa 1000  
atcttcaagg agatgaacaa tgcccttgct cacctacccc aaggggtgat 1050  
atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100  
atgtgaaaat tgtggactgg cttcctcaga gtgacccct ggctcaccca 1150  
agcatccgtc tgtttgtcac ccacggcggg cagaatagca taatggaggc 1200  
catccagcat ggtgtgccca tggtggggat ccctctctt ggagaccaggc 1250  
ctgaaaacat ggtccgagta gaagccaaaa agtttgggtt ttctattcag 1300  
ttaaagaagc tcaaggcaga gacattggct cttaagatga aacaaatcat 1350  
ggaagacaag agataacaagt ccgcggcagt ggctgccagt gtcatcctgc 1400  
gctcccaccc gtcagcccc acacagcggc tggtggctg gattgaccac 1450  
gtcctccaga cagggggcgc gacgcaccc aagccctatg tcttcagca 1500  
gccctggcat gagcagtacc tgttcgacgt ttttgtgtt ctgctgggc 1550  
tcactctggg gactctatgg ctttgggaa agctgctggg catggctgtc 1600  
tggtggctgc gtggggccag aaaggtgaag gagacataag gccaggtgca 1650  
gccttggcgg ggtctgtttg gtggcgatg tcaccatttc tagggagctt 1700  
cccactagtt ctggcagccc cattctctag tccttcttagt tatctcctgt 1750  
tttcttgaag aacagaaaa atggccaaaa atcatcctt ccacttgcta 1800  
attttgctac aaattcatcc ttactagctc ctgcctgcta gcagaaatct 1850  
ttccagtcct cttgtcctcc tttgtttgcc atcagcaagg gctatgctgt 1900  
gattctgtct ctgagtgact tggaccactg accctcagat ttccagcctt 1950  
aaaatccacc ttccctctca tgcgcctctc cgaatcacac cctgactctt 2000  
ccagcctcca tgtccagacc tagtcagcc ctctcaactcc tgcccctact 2050  
atctatcatg gaataacatc caagaaagac accttgcata ttcttcagt 2100  
ttctgttttgc ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150  
tgtgctttag agttcagggc cggacacagg ctcacaggc tccacattgg 2200  
gtccctgtct ctggtgccca cagtgagctc cttcttgct gagcaggcat 2250  
ggagactgta ggtttccaga tttcctgaaa aataaaagtt tacagcgtta 2300  
tctctccccca acctcactaa 2320

<210> 282  
<211> 523  
<212> PRT  
<213> Homo sapiens

<400> 282  
Met Ala Gly Gln Arg Val Leu Leu Leu Val Gly Phe Leu Leu Pro  
1 5 10 15  
Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr  
20 25 30  
Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile  
35 40 45  
Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg  
50 55 60  
Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln  
65 70 75  
Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys  
80 85 90  
Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly  
95 100 105  
Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln  
110 115 120  
Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys  
125 130 135  
Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys  
140 145 150  
Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile  
155 160 165  
Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro  
170 175 180  
Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met  
185 190 195  
Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe  
200 205 210  
Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile  
215 220 225  
Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu  
230 235 240  
Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe  
245 250 255  
Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly

260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn Pro	Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283

<211> 24

<212> DNA

<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 283  
tgccttgct cacctacccc aagg 24

<210> 284  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 284  
tcaggctggc ctccaaagag aggg 24

<210> 285  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 285  
cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 286  
gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50  
ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100  
cccgtcacac acacatacca tgttctccat ccccccaggt ccagccctca 150  
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200  
cgccctgg gcaggcggt tcattccctcc tttctctccc aaagcccaac 250  
tgctgtcact gcatgctctg ccaaggagga gggaaactgca gtgacagcag 300  
gagtaagagt gggaggcagg acagagctgg gacacaggtt tggagagggg 350  
gttcagcggag ccttagagagg gcagactatc agggtgccgg cggtgagaat 400  
ccagggagag gagcggaaac agaagagggg cagaagacccg gggcacttgt 450

gggtgcaga gcccctcagc catgttggga gccaaaggcac actggctacc 500  
aggcccccta cacagtcccg ggctgccctt ggttctggtg cttctggccc 550  
tggggcccg gtgggcccag gaggggtcag agcccgctt gctggagggg 600  
gagtgcctgg tggctgtga gcctggccga gctgctgcag gggggcccg 650  
gggagcagcc ctgggagagg cacccctgg gcgagtggca tttgctgcgg 700  
tccgaagcca ccaccatgag ccagcaggaa aaaccggcaa tggcaccagt 750  
ggggccatct acttcgacca ggtcctggtg aacgaggcg gtggcttga 800  
ccgggcctct ggctccttcg tagccctgt ccgggggtgtc tacagcttcc 850  
gttccatgt ggtgaaggta tacaaccgcc aaactgtcca ggtgagcctg 900  
atgctgaaca cgtggctgt catctcagcc tttgccaatg atcctgacgt 950  
gaccgggag gcagccacca gctctgtgtc actgcccattt gaccctgggg 1000  
accgagtgtc tctgcgcctg cgtcggggaa atctactggg tggttggaaa 1050  
tactcaagtt tctctggctt cctcatcttc cctctctgtc gacccaagtc 1100  
tttcaagcac aagaatccag cccctgacaa ctttcttctg ccctctcttg 1150  
ccccagaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200  
cctcttgca tgggaccctg tgccaaacac ccaagttaa gagaagagta 1250  
gagctgtggc atctccagac caggccttcc cacccaccca ccccccagtta 1300  
ccctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350  
ggcaaggaaa ggcaagaagg aagatctgca ctactttgcg gcctctgctc 1400  
ctccggttcc cccacccag cttcctgctc aatgctgatc agggacaggt 1450  
ggcgcaggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500  
cagcgtaccc tgcaggcttc ttccctgtgag gaaagccagc atcacggatc 1550  
tcagccagca ccgtcagaag ctgagccagc accgtatggg ctaggggtggg 1600  
aggctcagcc acaggcagaa gggtggaaag ggcctggagt ctgtggctgg 1650  
tgaggaagga aggagggtgt attgtctaga ctgaacatgg tacacattct 1700  
gcatgtatacg cagagcagcc agcaggtacg aatcctggct gtccttctat 1750  
gctggatccc agatggactc tggcccttac ctccccaccc gagattaggg 1800  
tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850  
ctggaagtgg accatggaaa acatcgataa ccatgcattcc tcttgcttgg 1900

ccacccctcg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950  
cactctgact gctgcctcct tcctcccagc tctctcactg agttatcttc 2000  
actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050  
gctgtcttat tctcctcctt aggcttccta ttacctggta ttccatgatt 2100  
cattccttca gaccctotcc tgccagtatg ctaaacccctc cctctctt 2150  
tcttatcccg ctgtcccatt ggcccagcct ggatgaatct atcaataaaa 2200  
caactagaga atgggtgtca gtgagacact atagaattac taaggagaag 2250  
atgcctctgg agtttggatc gggtgttaca ggtacaagta ggtatgtgc 2300  
agagggaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5					10					15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
					20				25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
					95				100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

170 175 180

Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser  
185 190 195

Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu  
200 205

<210> 288  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 288  
aggcagccac cagctctgtg ctac 24

<210> 289  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-27  
<223> Synthetic construct.

<400> 289  
cagagaggga agatgaggaa gccagag 27

<210> 290  
<211> 42  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-42  
<223> Synthetic construct.

<400> 290  
ctgtgctact gcccttggac cctggggacc gagtgtctgc 42

<210> 291  
<211> 1570  
<212> DNA  
<213> Homo sapiens

<400> 291  
gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50  
tagccgccccca gcctcgacgc cgtcccgaaa cccctgtgct ctgcgcgaag 100  
ccctggccccca gggggccgggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcccc gccgtgactg ggccggcttc agccatgaag accctcatag 200  
ccgcctactc cggggctctg cgccgcgagc gtcaggccga ggctgaccgg 250  
agccagcgct ctcacggagg acctgcgctg tcgcgcgagg ggtctggag 300  
atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350  
tcacacctggct caataggctc aaggtggaaa agcagctaca ggtcatctca 400  
gtgctccagt gggtcctgtc cttccttgta ctgggagtg cctgcagtgc 450  
catcctcatg tacatattct gcactgattg ctggctcatc gctgtgctct 500  
acttcacttg gctgggttt gactggaaaca caccaagaa aggtggcagg 550  
aggtcacagt gggtccgaaa ctgggctgtg tggcgctact ttgcagacta 600  
ctttcccatc cagctggtga agacacacaa cctgctgacc accaggaact 650  
atatcttgg ataccacccc catggtatca tgggcctggg tgccttctgc 700  
aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750  
gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800  
agtacctgat gtctggaggt atctgccctg tcagccggga caccatagac 850  
tatttgcctt caaagaatgg gagtggcaat gctatcatca tcgtggtcgg 900  
gggtgcggct gagtctctga gctccatgcc tggcaagaat gcagtcaccc 950  
tgccgaaccg caagggcttt gtgaaactgg ccctgcgtca tggagctgac 1000  
ctggttccca tctactcctt tggagagaat gaagtgtaca agcaggtgat 1050  
cttcgaggag ggctcctggg gccgatgggt ccagaagaag ttccagaaat 1100  
acattggttt cgccccatgc atcttccatg gtcgaggcct cttctcctcc 1150  
gacacctggg ggctggtgcc ctactccaag cccatcacca ctgttgtggg 1200  
agagcccatc accatccccca agctggagca cccaaacccag caagacatcg 1250  
acctgtacca caccatgtac atggaggccc tggtaagct ctgcacaag 1300  
cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350  
agccagcctt cggggccaat tccctggagg aaccagctgc aaatcacttt 1400  
tttgctctgt aaatttggaa gtgtcatggg tgtctgtggg ttattnaaaa 1450  
gaaattataa caatttgct aaaccaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550  
aaaaaaaaaa aaaaaaaaaa 1570

<210> 292  
<211> 388  
<212> PRT  
<213> Homo sapiens

<400> 292  
Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu  
1 5 10 15  
Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro  
20 25 30  
Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser  
35 40 45  
Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn  
50 55 60  
Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln  
65 70 75  
Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile  
80 85 90  
Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu  
95 100 105  
Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly  
110 115 120  
Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr  
125 130 135  
Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu  
140 145 150  
Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile  
155 160 165  
Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu  
170 175 180  
Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu  
185 190 195  
Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser  
200 205 210  
Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu  
215 220 225  
Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly  
230 235 240  
Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr  
245 250 255  
Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr		
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln		
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His		
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr		
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro		
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr		
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr		
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn		
380	385	

<210> 293  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 293  
gctgacacctgg ttcccatctta ctcc 24

<210> 294  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 294  
cccacagaca cccatgacac ttcc 24

<210> 295  
<211> 50  
<212> DNA  
<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 295

aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

ggcgccgcgg atggggcccg ggggcggcgg gcgcgcact cgctgaggcc 50

ccgacgcagg gccgggcggg gcccagggcc gaggagcgcg gcggccagag 100

cggggccgcg gaggcgcacgc cggggacgcc cgcgcgacga gcaggtggcg 150

gcggctgcag gcttgtccag ccggaagccc tgagggcagc tggcccact 200

ggctctgctg accttgcgtt ttggacggct gtccctcagcg agggggccgtg 250

cacccgctcc ttagcagcgc catgggcctg ctggccttcc tgaagaccca 300

gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggtctgg 350

tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400

cagctctacc gccgcctcaa ctggccgcctc gcctactcac tctggagcca 450

actggtcatg ctgctggagt ggtggtcctg cacggagtgt acactgttca 500

cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550

ctcaaccaca acttcgagat cgacttcctc tgtgggtggga ccatgtgtga 600

gcgccttcgga gtgctgggaa gctccaaggt cctcgctaag aaggagctgc 650

tctacgtgcc cctcatcgcc tggacgtggt actttctggta gattgtgttc 700

tgcaagcggaa agtgggagga ggaccgggac accgtggtcg aagggtcgag 750

gcgcctgtcg gactaccccg agtacatgtg gtttctctg tactgcgagg 800

ggacgcgttt cacggagacc aagcacgcgc ttagcatggta ggtggcggct 850

gctaaggggc ttccctgtcct caagtaccac ctgctgccgc ggaccaagg 900

cttcaccacc gcagtcaagt gcctccgggg gacagtgcga gctgtctatg 950

atgttaaccct gaacttcaga ggaaacaaga acccgccct gctggggatc 1000

ctctacggaa agaagtacga ggccggacatg tgcgtgagga gatttcctct 1050

ggaagacatc ccgctggatg aaaaggaagc agctcagtggtt cttcataaac 1100

tgtaccagga gaaggacgcgc ctccaggaga tatataatca gaagggtcgatg 1150

tttccagggg agcagttaa gcctgcccgg aggccgtgga ccctcctgaa 1200  
cttcctgtcc tggccacca ttctcctgtc tccccctcttc agttttgtct 1250  
tggcgtctt tgccagcggta tcacctctcc tgatcctgac tttcttgggg 1300  
tttgtggag cagttccctt tggagttcgc agactgata gagaatcgct 1350  
tgaacctggg aggtggagat tgcagtgagc tgagatggca tcactgtact 1400  
ccagcctagg caacagagca agactcagtc taaaaaaaaaaaaaaaacaa 1450  
aaaaaacccta gaaattctgg agttgaactg tgtagttact gacatgaaaa 1500  
attcactaga ggctgaacag cagatttgag cagggagaaa aaaatcagca 1550  
agcttgaaga tggcacccctt agattttca ggctaatgaa aaaagaatga 1600  
aggaaaatta acagcctcag agacccatgg tgcaccgtca cacaaatcaa 1650  
catatgcatg atgagagtcc cagaaggaga ggagagaaag ggtcagaaag 1700  
aatggccaca agctgatgaa aaacagtaac ctacccactc aggaagctca 1750  
gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800  
aatcaaagtg tcaaattgaca aagaatcttggaaagcagca gagatgagca 1850  
acttatcttggat ctttgatcag attaacagct catttctcct 1900  
cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950  
aaccttcaac tgtaatttggatggactttga gtcttagatg gtcctgac 2000  
cttgcgttcc agggacagtt ttcaattta atccctaata acaatttagtc 2050  
aagcttcctt gacctgttagg aaggcctgtc tttagggccgg gcacagtggc 2100  
ttacacctgt aatcccagca ctttgggagg cccagacggg tggatcattt 2150  
ggggtcaggc tgatctcaaa ctctgatcgtt caggtgatct gcccgcctca 2200  
gcctcccaa gtgttgtgat tgcaggcgtg agccactgctg cctggccgg 2250  
atttctttt aaggctgaat gatggggggcc aggcacgatg gctcacgcct 2300  
gtgatcccaa gtagcttggaa ttgtaaacat gcaccacat gcctggctaa 2350  
ttttgttatt tttagtagag acgtgttagc caggctggtc tcgatctcct 2400  
gacctcaagt gaccacactgc ctacgcctcc caaagtactg ggattacagg 2450  
cgtgagccac tggcctggc cttgagcatc ttgtgatgtg cttattggcc 2500  
atttgtatat ctcttatctt ctttggggaa atgtctgttc aagtcctttg 2550  
cctttttaaa tttttattat ttatattttt atttattttg agacagggtc 2600

ttgttctgtt gcccaggctg gagtacagtgc acagtcactgc 2650  
agcctcgacc tcctggctg cagtgcacccc cccacccatg cctcccttgt 2700  
agctgtatTT ttgttatTT tgatTTTgt agctgttagtt ttgttatTT 2750  
ttgtggagac agcatTTcac catgatgccc aggctggct tgaactcctg 2800  
agctcaagtgc atctgcctgc ttcaGCCTCC caaagtgcgt ggattacaga 2850  
catgagccac tgcacCTGGC aaactccaa aattcaacac acacacacaa 2900  
aaaaccacct gattcaaaat gggcagaggg gcccgggtgtg gcccccaacta 2950  
ccagggagac tgaagtggga ggatcgcttg ggcattgagaa gtcgaggctg 3000  
cagtgagtcg aggttgcgc actgcattcc agcctggaca acagagttag 3050  
accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu  
1 5 10 15

Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe  
20 25 30

Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu  
35 40 45

Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln  
50 55 60

Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu  
65 70 75

Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala  
80 85 90

Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly  
95 100 105

Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val  
110 115 120

Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr  
125 130 135

Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu  
140 145 150

Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr  
155 160 165

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe
				170					175					180
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys
				185					190					195
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly
				200					205					210
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val
				215					220					225
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu
				230					235					240
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val
				245					250					255
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala
				260					265					270
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln
				275					280					285
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys
				290					295					300
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala
				305					310					315
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe
				320					325					330
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val
				335					340					345
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu
				350					355					360
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln							
				365										

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt gggtgacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299  
gccacacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300  
ccaaggtcct cgctaagaag gagctgtct acgtgcccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301  
gatattcttt attttaaga atctgaagta ctatgcatca ctccctccaa 50  
tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gttttcttt 100  
tgcttagca ctggggcaact tcttgcttat ttctttggta ggaaaggggc 150  
tcagttgtc ttgtggggtt ggtggcaggc aggccggctt acgcctgata 200  
cggccctggg ttagaaggga aggaaagata aactttata caaatgggg 250  
tagctggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300  
ataccttctt ttctctaacc tggcataaccc tgcttaaagc ctctcagggc 350  
ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400  
gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450  
tgtcgccct gtaatgtggt atgccatggg gtcttcac aagccttcc 500  
tctttggctg gacactgttc cctggccccc ccatactttt cctacttaat 550  
atgttagtcat cctgcagatt tcaattctaa catcatttc tccagggatc 600  
ctggcctgac agaatctcat cttgttaat gctctcataa gaccacttgt 650  
ttccctttg cagcacttgc cactcagttg tatctttatg tgcgttgcgtg 700  
gttgtatggg ttgtgtctgt tccccagaat gcccagctct gagctgcgtg 750

agggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800  
ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850  
aaatctctca gttcaccaga tggtgttaggg cccagcattg taaattcaca 900  
cgttgactgt gcttgtgaat tatctgggg tgcaggtcct gattcagtag 950  
gcccagggttg ggcatctcta acaaactccc acgtgatgct gatgctggtc 1000  
ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050  
tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgatc 1100  
acctggagtc aggattcaa gactagcctg gccaaacatgg tggaacccca 1150  
tctgtactaa aaatacacaa attagctgg catggtgca catgcctgta 1200  
gtcccagcta cttgggaggc tgaagcaaga gaatcgctt aacctggag 1250  
gcggagggttg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300  
acagagttag actctatgtc caaaaaaaaaaaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile  
1 5 10 15

His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe  
20 25 30

Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly  
35 40 45

Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val  
50 55 60

Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp  
65 70 75

Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr  
80 85 90

Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln  
95 100 105

Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu  
110 115 120

Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr  
125 130 135

Cys Gly Val Leu Leu Ser Phe Leu

<210> 303  
<211> 1768  
<212> DNA  
<213> Homo sapiens

<400> 303  
ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50  
aagggtgtgt gattatagggt gtaagccacc gtgtctggcc tctgaacaac 100  
tttttcagca actaaaaaaag ccacaggagt tgaactgcta ggattctgac 150  
tatgctgtgg tggcttagtgc tcctactcct acctacatta aaatctgttt 200  
tttggttctct tgtaacttagc ctttacccctc ctaacacaga ggatctgtca 250  
ctgtggctct ggcccaaacc tgaccccac tctggaacga gaacagaggt 300  
ttctacccac accgtccccct cgaagccggg gacagcctca ctttgctggc 350  
ctctcgctgg agcagtgccccc tcaccaactg tctcacgtct ggaggcactg 400  
actcgggcag tgcaggtagc tgagcctttt ggtagctgcg gctttcaagg 450  
tgggccttgc cctggccgta gaagggattt acaagcccga agatttcata 500  
ggcgatggct cccactgccc aggcatcagc cttgctgttag tcaatcactg 550  
ccctggggcc aggacgggccc gtggacacct gctcagaagc agtgggttag 600  
acatcacgct gcccggccat ctaacctttt catgtcctgc acatcacctg 650  
atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700  
gctgtggctc agacccagaa ggggtctgt tagaccacct ggtttatgtg 750  
acaggacttg catttccttg gaacatgagg gaacgcccga ggaaagcaaa 800  
gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850  
gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900  
ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc 950  
atcagacagc cggttccgccc ccgatccacg taccagctgc tgaaggcua 1000  
ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgtca 1050  
ccagccaggc gcagccgtct gggaggagc aagcaaagtg accatttctc 1100  
ctccccctcct tccctctgag aggcctcct atgtccctac taaagccacc 1150  
agcaagacat agctgacagg ggctaatggc tcagtgttgg cccaggaggt 1200  
cagcaaggcc tgagagctga tcagaaggc ctgctgtgcg aacacggaaa 1250

tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300  
ctcaatttaa atcatgttct agtaattgga gctgtccccca agaccaaagg 1350  
agcttagagct tggttcaaata gatctccaag ggcccttata ccccaggaga 1400  
ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccaggtgcat 1450  
taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacatttgg 1500  
gaggccgagg cgggtagatc acctgaggc aggagttcaa gaccagcctg 1550  
gccaacatgg tgaaaccct gtctctacta aaaataaaaaaaaactagcc 1600  
aggcatggtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650  
gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700  
ttcagcctga gcaacacagc gagactctgt ctcagaaaaataaaaaaaag 1750  
aattatggtt atttgtaa 1768

<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser	
1					5				10				15	
Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
					20				25				30	
Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
					35				40				45	
Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50				55					60	
Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
					65				70				75	
Thr	Val	Ser	Arg	Leu	Glu	Ala	Leu	Thr	Arg	Ala	Val	Gln	Val	Ala
				80				85					90	
Glu	Pro	Leu	Gly	Ser	Cys	Gly	Phe	Gln	Gly	Gly	Pro	Cys	Pro	Gly
				95				100					105	
Arg	Arg	Arg	Asp											

<210> 305

<211> 989

<212> DNA

<213> Homo sapiens

<400> 305

gcgggcccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50  
tgtcactgcc tccccccgc tcctgcccgc gccatgaccc agccggtgcc 100  
ccggctctcc gtccccggcg cgctggccct gggctcagcc gcactggcg 150  
ccgccttcgc cactggcctc ttctgggga ggccgtgccc cccatggcga 200  
ggccggcgag agcagtgcct gcttccccc gaggacagcc gcctgtggca 250  
gtatcttctg agccgctcca tgccggagca cccggcgctg cgaagcctga 300  
ggctgctgac cctggagcag ccgcaggggg attctatgtat gacctgcgag 350  
caggcccagc tcttggccaa cctggcgccgg ctcatccagg ccaagaaggc 400  
gctggacctg ggcacccctca cgggctactc cgcctggcc ctggccctgg 450  
cgctgcccgc ggacgggcgc gtgggtaccc gcgaggtgga cgccgagccc 500  
ccggagctgg gacggccctt gtggaggcag gccgaggcg agcacaagat 550  
cgacctccgg ctgaagcccg cttggagac cttggacgag ctgctggcg 600  
cggcgaggc cggcacccctc gacgtggccg tggatgc ggacaaggag 650  
aactgctccg cctactacga gcgctgcctg cagctgctgc gacccggagg 700  
catcctcgcc gtcctcagag tcctgtggcg cggaaagggtg ctgcaacctc 750  
cgaaaggaga cgtggcgcc gagtgtgtgc gaaacctaaa cgaacgcata 800  
cgccggacg tcagggtcta catcagcctc ctgcctggc gcgatggact 850  
caccttggcc ttcaagatct aggctggcc cctagtgagt gggctcgagg 900  
gagggttgcc tggaaacccc aggaattgac cctgagttt aaattcgaaa 950  
ataaaagtggg gctggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Ileu	Ser	Val	Pro	Ala	Ala	Ileu	Ala
1				5					10				15	
Lleu	Gly	Ser	Ala	Ala	Ileu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Ileu	Phe
					20				25				30	
Lleu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35				40				45		
Lleu	Lleu	Pro	Pro	Glu	Asp	Ser	Arg	Ileu	Trp	Gln	Tyr	Ileu	Ileu	Ser
				50				55				60		

Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu
														65
														70
														75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln
														80
														85
														90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys
														95
														100
														105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu
														110
														115
														120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val
														125
														130
														135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala
														140
														145
														150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu
														155
														160
														165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp
														170
														175
														180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr
														185
														190
														195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val
														200
														205
														210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly
														215
														220
														225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg
														230
														235
														240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly
														245
														250
														255
Leu	Thr	Leu	Ala	Phe	Lys	Ile								
														260

<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

ccggccgcgc agccgctacc gccgctgcag ccgcgttccg cggcctggc 50

ctctcgccgt cagcatgccca cacgccttca agccccggga ctgggttttc 100

gctaaatgttta agggctaccc tcactggcct gccaggatcg acgacatcgc 150

ggatggcgcc gtgaagcccc cacccaacaa gtacccatc tttttttttt 200

gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300  
agggctgtgg gagatccaga acaaccccca cgccagctac agcgcccctc 350  
cgccagttag ctcctccgac agcgaggccc ccgaggccaa ccccgccgac 400  
ggcagtgacg ctgacgagga cgatgaggac cggggggtca tggccgtcac 450  
agcggttaacc gccacagctg ccagcgacag gatggagagc gactcagact 500  
cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta 550  
aagatgtcggt tctcgaaacg agcccgaaag gcctccagcg acctggatca 600  
ggccagcgtg tccccatccg aagaggagaa ctcggaaagc tcatactgagt 650  
cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc 700  
cgggcgccac ggagggggccc tctgggggga cggaaaaaaa agaaggcgcc 750  
gtcagcctcc gactccgact ccaaggccga ttccggacggg gccaagcctg 800  
agccgggtggc catggcgccgg tcggcgtcct cctccctcctc ttccctcctcc 850  
tcctccgact ccgatgtgtc tgtgaagaag cctccgaggg gcaggaagcc 900  
agcggagaag cctctcccgaa agcccgagg gcggaaaccg aagcctgaac 950  
ggcctccgtc cagctccagc agtgcacagt acagcgacga ggtggaccgc 1000  
atcagtgagt ggaagcggcg ggacgaggcg cggaggcgagc agctggaggc 1050  
ccggcggcgg cgagagcagg aggaggagct gcggcgcctg cgggagcagg 1100  
agaaggagga gaaggagcgg aggcgcgagc gggccgaccg cggggaggct 1150  
gagcggggca gcggcggcag cagcggggac gagtcaggg aggacgatga 1200  
gcccgtaag aagcggggac gcaaggcccg gggccgggt ccccgctcct 1250  
cctctgactc cgagcccgag gccgagctgg agagagaggc caagaaatca 1300  
gcgaagaagc cgcaagtccctc aagcacagag cccgccagga aacctggcca 1350  
gaaggagaag agagtgcggc ccgaggagaa gcaacaagcc aagccgtga 1400  
aggtggagcg gacccggaag cggtccgagg gcttctcgat ggacaggaag 1450  
gtagagaaga agaaagagcc ctccgtggag gagaagctgc agaagctgca 1500  
cagttagatc aagtttgcgg taaagggtcga cagccggac gtgaagaggt 1550  
gcctgaatgc cctagaggag ctggaaaccc tgcaggtgac ctctcagatc 1600  
ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttccgggtta 1650  
caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tatacccgcc 1700

tcaagtcgct ggtcctcgcc ccaaagatcg aggccgtgc gaaagtgaac 1750  
aaggctggta tggagaagga gaaggccgag gagaagctgg ccggggagga 1800  
gctggccggg gaggaggccc cccaggagaa ggcggaggac aagcccagca 1850  
ccgatctctc agccccactg aatggcgagg ccacatcaca gaagggggag 1900  
agcgcagagg acaaggagca cgaggagggt cggactcgg aggaggggcc 1950  
aagggtggc tcctctgaag acctgcacga cagcgtacgg gagggtccc 2000  
acctggacag gcctgggagc gaccggcagg agcgcgagag ggcacgggg 2050  
gactcggagg ccctggacga ggagagctga gccgcggca gccaggccc 2100  
gccccggccc gagctcaggc tgccccctc cttccccgc tcgcaggaga 2150  
gcagagcaga gaactgtggg gaacgctgtg ctgttgtat ttgtccctt 2200  
gggtttttt ttcctgccta atttctgtga tttccaacca acatgaaatg 2250  
actataaacg gtttttaat ga 2272

<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met Pro His Ala Phe Lys Pro Gly Asp Leu Val Phe Ala Lys Met  
1 5 10 15

Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Asp Ile Ala Asp  
20 25 30

Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe  
35 40 45

Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro  
50 55 60

Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys  
65 70 75

Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala  
80 85 90

Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala  
95 100 105

Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp  
110 115 120

Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala  
125 130 135

Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Lys Ser Ser

	140	145	150
Asp Asn Ser Gly	Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met	Ser
155	160	165	
Val Ser Lys Arg Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln Ala		
170	175	180	
Ser Val Ser Pro Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser Glu		
185	190	195	
Ser Glu Lys Thr Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys Ala		
200	205	210	
Ala Val Arg Ala Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys Lys		
215	220	225	
Lys Lys Ala Pro Ser Ala Ser Asp Ser	Lys Ala Asp Ser		
230	235	240	
Asp Gly Ala Lys Pro Glu Pro Val Ala	Met Ala Arg Ser Ala Ser		
245	250	255	
Ser Ser Ser Ser Ser Ser Ser Asp	Ser Asp Val Ser Val		
260	265	270	
Lys Lys Pro Pro Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu Pro		
275	280	285	
Lys Pro Arg Gly Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser Ser		
290	295	300	
Ser Ser Ser Asp Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser Glu		
305	310	315	
Trp Lys Arg Arg Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala Arg		
320	325	330	
Arg Arg Arg Glu Gln Glu Glu Leu Arg	Arg Leu Arg Glu Gln		
335	340	345	
Glu Lys Glu Glu Lys Glu Arg Arg Glu	Arg Ala Asp Arg Gly		
350	355	360	
Glu Ala Glu Arg Gly Ser Gly Gly Ser	Gly Asp Glu Leu Arg		
365	370	375	
Glu Asp Asp Glu Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg Gly		
380	385	390	
Arg Gly Pro Pro Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu Leu		
395	400	405	
Glu Arg Glu Ala Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser Ser		
410	415	420	
Thr Glu Pro Ala Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val Arg		
425	430	435	

Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr
								440		445				450
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys
				455					460					465
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser
				470					475					480
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg
				485				490						495
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser
				500				505						510
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys
				515				520						525
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala
				530				535						540
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile
				545				550						555
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys
				560				565						570
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala
				575				580						585
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala
				590				595						600
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu
				605				610						615
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg
				620				625						630
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro
				635				640						645
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala
				650				655						660
Arg	Gly	Asp	Ser	Glu	Ala	Leu	Asp	Glu	Glu	Ser				
				665				670						

<210> 309  
<211> 3871  
<212> DNA  
<213> Homo sapiens

<400> 309  
gttggttctc ctggatcttc accttaccaa ctgcagatct tggactcat 50  
cagcctcaat aattatatta aatataacacc atttgaaaga gaacattgtt 100

ttcatcatga atgctaataa agatgaaaga cttaaagcca gaagccaaga 150  
tttcacctt ttccctgctt tgatgtatgc aagcatgacc atgttgttc 200  
ttccagtcac tggcacattt aagcaaaata ttccaagact caagctaacc 250  
tacaaagact tgctgcttc aaatagctgt attcccttt tggttcatc 300  
agaaggactg gatTTcaaa ctccctctt agatgaggaa agaggcaggc 350  
tgctcttggg agccaaagac cacatcttc tactcagtct ggttgactta 400  
aacaaaaatt ttaagaagat ttattggcct gctgcaaagg aacgggtgga 450  
attatgtaaa ttagctgggaa aagatgccaa tacagaatgt gcaaattca 500  
tcagagtact tcagccctat aacaaaactc acatatatgt gtgtggaact 550  
ggagcatttc atccaatatg tggtatatt gatcttggag tctacaagga 600  
ggatattata ttcaaactag acacacataa tttggagtct ggcagactga 650  
aatgtccttt cgatcctcag cagcctttt cttcagtaat gacagatgag 700  
tacctctact ctggaacagc ttctgatttc cttggcaaag atactgcatt 750  
cactcgatcc ctgggccta ctcatgacca ccactacatc agaactgaca 800  
tttcagagca ctactggctc aatggagcaa aatttattgg aactttcttc 850  
ataccagaca cctacaatcc agatgatgtat aaaaatatt tcttcttcg 900  
tgaatcatct caagaaggca gtaccccgaa taaaaccatc ctttctcgag 950  
ttggaagagt ttgtaagaat gatgttaggag gacaacgcag cctgataaac 1000  
aagtggacga cttttcttaa ggccagactg atttgctcaa ttccctggaag 1050  
tgatggggca gatacttact ttgatgagct tcaagatatt tatttactcc 1100  
ccacaagaga tgaaagaaat cctgttagtat atggagtctt tactacaacc 1150  
agctccatct tcaaaggctc tgctgttgt gtgtatagca tggctgacat 1200  
cagagcagtt tttaatggtc catatgctca taaggaaagt gcagaccatc 1250  
gttgggtgca gatgtatggg agaattcctt atccacggcc tggtagatgt 1300  
ccaagcaaaa cctatgaccc actgattaag tccacccgag attttccaga 1350  
tgatgtcatc agttcataa agcggcactc tgtgtatgtat aagtccgtat 1400  
accagggtgc aggaggacca acgttcaaga gaatcaatgt ggattacaga 1450  
ctgacacaga tagtggtgga tcatgtcatt gcagaagatg gccagtgacg 1500  
tgtaatgttt cttggAACAG acattggAACAC tgcctcaaa gttgtcagca 1550

tttcaaagga aaagtggaaat atggaagagg tagtgctgga ggagttgcag 1600  
atattcaagc actcatcaat catcttgaac atggaattgt ctctgaagca 1650  
gcaacaattg tacattgggtt cccgagatgg attagttcag ctctccttgc 1700  
acagatgcga cacttatggg aaagcttgcg cagactgttgc tcttgcaga 1750  
gaccctact gtgcctggga tggaaatgca tgctctcgat atgctcctac 1800  
ttctaaaagg agagctagac gccaagatgt aaaatatggc gacccaatca 1850  
cccagtgctg ggacatcgaa gacagcatta gtcatgaaac tgctgatgaa 1900  
aagggtgattt ttggcattga atttaactca acctttctgg aatgtataacc 1950  
taaatcccaa caagcaacta ttaaatggta tatccagagg tcagggatg 2000  
agcatcgaga ggagttgaag cccgatgaaa gaatcatcaa aacggaatat 2050  
gggctactga ttcaagatctt gcagaagaag gattctggta tgtattactg 2100  
caaagcccag gagcacactt tcatccacac catagtgaag ctgactttga 2150  
atgtcattga gaatgaacag atgaaaata cccagaggc agagcatgag 2200  
gaggggcagg tcaaggatct attggctgag tcacggttga gatacaaaga 2250  
ctacatccaa atccttagca gcccaaactt cagcctcgac cagttactg 2300  
aacagatgtg gcacagggag aagcggagac agagaaacaa gggggccca 2350  
aagtggaaagc acatgcagga aatgaagaag aaacgaaatc gaagacatca 2400  
cagagacctg gatgagctcc ctagagctgt agccacgtag ttttctactt 2450  
aatttaaaga aaagaattcc ttacctataa aaacattgcc ttctgtttg 2500  
tataccctt atagtaattc ataaatgctt cccatggagt tttgctaagg 2550  
cacaagacaa taatctgaat aagacaatat gtgatgaata taagaaagg 2600  
caaaaaattc atttgaacca gtttccaag aacaaatctt gcacaagcaa 2650  
agtataagaa ttatcctaaa aataggggtt ttacagttgt aaatgtttta 2700  
tgttttgagt tttggaaattt attgtcatgt aaatagttga gctaaagcaag 2750  
ccccgaattt gatagtgtat aaggtgcttt attccctcgat atgtccattt 2800  
agcatggaat ttaccatgca gtttgctat gttcttatga acagatataat 2850  
cattcctatt gagaaccagc tacttgtgg taggaaataa gaggtcagac 2900  
acaaattaag acaactccca ttatcaacag gaactttctc agtgagccat 2950  
tcactcctgg agaatggat aggaatttgg agaggtgcat tatttcttc 3000

tggccactgg ggttaaattt agtgtactac aacattgatt tactgaaggg 3050  
cactaatgtt tcccccaagga tttctattga ctagtcagga gtaacaggtt 3100  
cacagagaga agttggtgct tagttatgtg ttttttagag tatatactaa 3150  
gctctacagg gacagaatgc ttaataaata cttaataag atatggaaa 3200  
atatttaat aaaacaagga aaacataatg atgtataatg catcctgatg 3250  
ggaaggcatg cagatggat ttgttagaag acagaaggaa agacagccat 3300  
aaattctggc tttggggaaa actcatatcc ccatgaaaag gaagaacaat 3350  
cacaataaaa gtgagagtaa tgtaatggag ctctttcac tagggtataa 3400  
gtagctgcc aattttaatt catctgttaa aaaaaatcta gattataaca 3450  
aactgctagc aaaatctgag gaaacataaa ttcttctgaa gaatcatagg 3500  
aagagtagac attttattta taaccaatga tatttcagta tatattttct 3550  
ctctttaaa aaatatttat catactctgt atatttttc ttttactgc 3600  
ctttattctc tcctgtatat tggattttgt gattatattt gagtgaatag 3650  
gagaaaacaa tatataacac acagagaatt aagaaaatga catttctggg 3700  
gagtggggat atatatttgt tgaataacag aacgagtgt aatttttaac 3750  
aacggaaagg gttaaattaa ctcttgaca tcttcactca acctttctc 3800  
attgctgagt taatctgttg taattgttagt attgttttg taatttaaca 3850  
ataaataaagc ctgctacatg t 3871

<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

Met	Asn	Ala	Asn	Lys	Asp	Glu	Arg	Leu	Lys	Ala	Arg	Ser	Gln	Asp
1				5				10					15	

Phe	His	Leu	Phe	Pro	Ala	Leu	Met	Met	Leu	Ser	Met	Thr	Met	Leu
				20				25					30	

Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35				40					45	

Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro	
				50				55					60	

Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65				70					75	

Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80	85	90
Phe Leu Leu Ser Leu Val Asp Leu Asn Lys	Asn Phe Lys Lys Ile	
95	100	105
Tyr Trp Pro Ala Ala Lys Glu Arg Val Glu	Leu Cys Lys Leu Ala	
110	115	120
Gly Lys Asp Ala Asn Thr Glu Cys Ala Asn	Phe Ile Arg Val Leu	
125	130	135
Gln Pro Tyr Asn Lys Thr His Ile Tyr Val	Cys Gly Thr Gly Ala	
140	145	150
Phe His Pro Ile Cys Gly Tyr Ile Asp Leu	Gly Val Tyr Lys Glu	
155	160	165
Asp Ile Ile Phe Lys Leu Asp Thr His Asn	Leu Glu Ser Gly Arg	
170	175	180
Leu Lys Cys Pro Phe Asp Pro Gln Gln	Pro Phe Ala Ser Val Met	
185	190	195
Thr Asp Glu Tyr Leu Tyr Ser Gly Thr Ala	Ser Asp Phe Leu Gly	
200	205	210
Lys Asp Thr Ala Phe Thr Arg Ser Leu	Gly Pro Thr His Asp His	
215	220	225
His Tyr Ile Arg Thr Asp Ile Ser Glu His	Tyr Trp Leu Asn Gly	
230	235	240
Ala Lys Phe Ile Gly Thr Phe Phe Ile Pro	Asp Thr Tyr Asn Pro	
245	250	255
Asp Asp Asp Lys Ile Tyr Phe Phe Arg	Glu Ser Ser Gln Glu	
260	265	270
Gly Ser Thr Ser Asp Lys Thr Ile Leu	Ser Arg Val Gly Arg Val	
275	280	285
Cys Lys Asn Asp Val Gly Gly Gln Arg	Ser Leu Ile Asn Lys Trp	
290	295	300
Thr Thr Phe Leu Lys Ala Arg Leu Ile	Cys Ser Ile Pro Gly Ser	
305	310	315
Asp Gly Ala Asp Thr Tyr Phe Asp Glu	Leu Gln Asp Ile Tyr Leu	
320	325	330
Leu Pro Thr Arg Asp Glu Arg Asn Pro	Val Val Tyr Gly Val Phe	
335	340	345
Thr Thr Thr Ser Ser Ile Phe Lys Gly	Ser Ala Val Cys Val Tyr	
350	355	360
Ser Met Ala Asp Ile Arg Ala Val Phe	Asn Gly Pro Tyr Ala His	
365	370	375

Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile  
                   380                  385                  390  
 Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro  
                   395                  400                  405  
 Leu Ile Lys Ser Thr Arg Asp Phe Pro Asp Asp Val Ile Ser Phe  
                   410                  415                  420  
 Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala  
                   425                  430                  435  
 Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr  
                   440                  445                  450  
 Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp  
                   455                  460                  465  
 Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val  
                   470                  475                  480  
 Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu  
                   485                  490                  495  
 Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu  
                   500                  505                  510  
 Leu Ser Leu Lys Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly  
                   515                  520                  525  
 Leu Val Gln Leu Ser Leu His Arg Cys Asp Thr Tyr Gly Lys Ala  
                   530                  535                  540  
 Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp  
                   545                  550                  555  
 Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala  
                   560                  565                  570  
 Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp  
                   575                  580                  585  
 Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val  
                   590                  595                  600  
 Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro  
                   605                  610                  615  
 Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly  
                   620                  625                  630  
 Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys  
                   635                  640                  645  
 Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser  
                   650                  655                  660  
 Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr

665	670	675
Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu		
680	685	690
Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu		
695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu		
710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp		
725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp		
740	745	750
Lys His Met Gln Glu Met Lys Lys Arg Asn Arg Arg His His		
755	760	765
Arg Asp Leu Asp Glu Leu Pro Arg Ala Val Ala Thr		
770	775	

```

<210> 311
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 311
 caacgcagcc gtgataaaca agtgg 25

<210> 312
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 312
 gcttggacat gtaccaggcc gtgg 24

<210> 313
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

```

<400> 313  
ggccagactg atttgctcaa ttcttggaa tgatggggca gatac 45  
  
<210> 314  
<211> 3934  
<212> DNA  
<213> Homo sapiens  
  
<400> 314  
ccctgaccc cctgagccac actgagctgg aagccgcaga ggtcatcctg 50  
gagcatgccc accgcgggga gcagacaacc tcccaggtaa gctgggagca 100  
agacctgaag ctgttttttc aggagcctgg tgtattttcc cccacccac 150  
ctcagcagtt tcagccagca gggactgatc aggtgtgtgt cctggagtgg 200  
ggagcagaag gcgtggctgg caagagtggc ctggagaaag agttcagcg 250  
cttgaccagc cgagctgccc gtgactacaa gatccagaac catggcatc 300  
gggtgaggtg gggggcaca ggtgtcatgt gcacacctt gtctcagcaa 350  
gaagagctga gagagggat cttggagcca ttgagggtgt catggagcta 400  
cagagggag ggaaaggat tttaaaggtaa cagtgtggca caatagttaa 450  
gagcacagtt tttggagcta gaccgacata gttcaattt ctctctgtt 500  
gtttcctagt tctgttagccc caggttaagg agtacttaa cctctctgg 550  
cttcaatttc ctcatcacta aagttagggcc aataatagca cccacccat 600  
agggaaagatt aaatgacata atgtatgtga tgcaacttagc aaagtaccag 650  
tcccatagta agtcatgccc cacagtattt ccacccaccc ctgttctctg 700  
cctccccaac caggtactgc aacgactggc gcagaggcgg cagcaggctt 750  
cagagcggga ggctccaagc atagaacaga gttacagga agtgcgagag 800  
agcatccgcc gggcacaggt gagccaggtg aagggggctg cccggctggc 850  
cctgctgcag gggctggct tagatgtggc gctggctggc aagccagcca 900  
tgacccaggc ccaggatgag gtggagcagg agcggccggct cagtgaggct 950  
cggtgtcccc agagggaccc ctctccaacc gctgaggatg ctgagcttc 1000  
tgactttgag gaatgtgagg agacgggaga gcttttgag gagectggcc 1050  
cccaagccct ggccacgagg gccctccctt gccctgcaca cgtggatattt 1100  
cgctatcagg cagggcgtga ggatgagctg acaatcacgg agggtgagtg 1150  
gctggaggc atagaggagg gagatgctga cgaatgggtc aaggctcgga 1200  
accagcacgg cgaggttaggc tttgtccctg agcgatatct caacttcccg 1250

gacctctccc tcccagagag cagccaagac agtgacaatc cctgcggggc 1300  
agagcccaaca gcattcctgg cacaggccct gtacagctac accggacaga 1350  
gtcgagagga gctgagcttc cctgaggggg cactcatccg tctgctgcc 1400  
cggcccaag atggagtata tgacggcttc tggaggggag aatttgggg 1450  
ccgtgttggg gtcttccct ccctgctggt ggaagagctg ctggccccc 1500  
cagggccacc tgaactctct gaccctgaac agatgctgcc gtccccc 1550  
cctcccaagct tctccccacc tgcacctacc tctgtgttgg atggggccc 1600  
tgcacctgtc ctgcctggg acaaagccct ggacttccct gggttcctgg 1650  
acatgatggc acctcgactc aggccgatgc gtccaccacc tccccggcc 1700  
gctaaagccc cgatcctgg ccacccagat cccctcacct gaaggccagg 1750  
gaagccttga cccccagtga tgctgctgtc cctatcttca agctgtcaga 1800  
ccacaccatc aatgatccag agcaacacag ccaaaagctg gaatgccct 1850  
tatttccacc ctcaccccca agggtgaaa cttgcccatt cccatttcta 1900  
gagctggaac ccactccctt tttccatt gttctatcat ctctaggacc 1950  
ggaactacta cttctcttc tgtcatgacc ctatctaggg tggtgaaatg 2000  
cctgaaatct ctggggctgg aaaccatcca tcaaggcttc tagtagttct 2050  
ggcccaccc tttccccacc ctggctccat gacccacccc actctggatg 2100  
ccagggtcac tgggttggg ctggggagag gaacaggcct tggaatcag 2150  
gagctggagc caggatgcga agcagctgta atggtctgag cgattttatt 2200  
gacaatgaat aaagggcacg aaggccaggc cagggcctgg gcctttgtg 2250  
ctaagagggc agggggccta cggtgctatt gctttagggg cccaccacgg 2300  
gcaggggcct gctccagct gccacgctct atcatatgga gcgagggttt 2350  
gggaaaggcg gggcaggcag cctgttgcaag gcaggggaag gagaagagac 2400  
tgaggggctg tgacctctcc tgaggccccc agcctgagac tgtgcaactc 2450  
caggtggaaag tagagctggt ccctcagctg gggggcagtg ctgtccagtg 2500  
gaggggaggg cttcacgcc caccacccc ctggccctgc cagctggtag 2550  
tccatcagca caatgaagga gacttggaga agaggaagaa taacactgtt 2600  
gcttcctgtt caagctgtt ccagctttc ccctggggct ccaggacctt 2650  
ccctacccctt accacccaaac caaggattt atagcaaagg ctaaggctgc 2700

agtttactct gggggttcag ggagccgaaa ggcttaaata gttaagtag 2750  
gtgatggaa gatgagatta cctcatttag ggctcaggca gactcaccc 2800  
acatactccc tgctccctgt ggttagagaca cctgagagaa aggggagggg 2850  
tcaacaatga gagaccagga gtaggtccta tcagtcccc ccagagtaga 2900  
gagaataag agcccagccc agtgcagtcc cggtgtgtt ttcctacctg 2950  
gtgatcagaa gtgtctggtt tgcttggctg cccatttgcc tcttgagtgg 3000  
gcagccctgg gcttgggccc ctccctccgg ccctcagtgt tggctctgca 3050  
gaagctctgg gttcccttc aagtgcacga ggggttaggc tgctgtccct 3100  
gagtcctcca ttctgtactg gggggctggc taggacctgg ggctgtggcc 3150  
tctcaggggg cagcctctcc atggcaggca tccctgcctt gggctgcct 3200  
cccccagacc cctgaccacc ccctgggtcc tgtccccac cagagcccc 3250  
gctcctgtct gtggggagc catcacggtg ttctgtcgagt ccatacgct 3300  
tctcaatgtg tgtcacccgg aacctggag gggagggAAC actggggTTT 3350  
aggaccacaa ctcagaggct gcttggccct cccctctgac cagggacatc 3400  
ctgagttgg tggctacttc cctctggcct aaggtagggg aggcttctc 3450  
agattgtgg gcacattgtg tagcctgact tctgctggag ctcccagtcc 3500  
aggagggaaAG agccaaggcc cactttggg atcaggtgcc tgatcactgg 3550  
gccccctacc tcagcccccc ttccctgga gcacctgccc cacctgcccc 3600  
cagagaacac agtggctcc cctgtccggg ggcggcttt tccttccttg 3650  
gagcgtccct gacggacaag tggaggcctc ttgctgcggc tgcaatggat 3700  
gcaaggggct gcagagcccc ggtgcactgt gtgatgatgg gagggggctc 3750  
cgtcctgcag gctggaggtg gcatccacac tggacagcag gaggagggga 3800  
gtgagggtaa catttccatt tcccttcatt tttgtttct tacgttcttt 3850  
cagcatgctc cttaaaaccc cagaagcccc aatttccccca agccccattt 3900  
tttcttgtct ttatctaata aactcaatat taag 3934

<210> 315  
<211> 370  
<212> PRT  
<213> Homo sapiens

<400> 315  
Met Gln Leu Ala Lys Tyr Gln Ser His Ser Lys Ser Cys Pro Thr  
1 5 10 15

Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu
						20			25				30	
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala
						35			40				45	
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg
						50			55				60	
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu
						65			70				75	
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala
						80			85				90	
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser
						95			100				105	
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp
						110			115				120	
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu
						125			130				135	
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro
						140			145				150	
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp
						155			160				165	
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu
						170			175				180	
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu
						185			190				195	
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser
						200			205				210	
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu
						215			220				225	
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln
						230			235				240	
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu
						245			250				255	
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly
						260			265				270	
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu
						275			280				285	
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu
						290			295				300	
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala

305	310	315
Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly 320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro 335	340	345
Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Ala Lys Ala 350	355	360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr 365	370	
<210> 316		
<211> 4407		
<212> DNA		
<213> Homo sapiens		
<400> 316		
cacagggaga cccacagaca catatgcacg agagagacag aggaggaaag 50		
agacagagac aaaggcacag cggaagaagg cagagacagg gcagggcacag 100		
aagcggccca gacagagtcc tacagaggga gaggccagag aagctgcaga 150		
agacacaggc agggagagac aaagatccag gaaaggaggg ctcaggagga 200		
gagtttggag aagccagacc cctggcacc tctcccaagc ccaaggacta 250		
agttttctcc atttcctta acggtcctca gcccttctga aaactttgcc 300		
tctgaccttg gcaggagtcc aagccccag gctacagaga ggagcttcc 350		
aaagcttaggg tgtggaggac ttggtgccct agacggcctc agtccctccc 400		
agctgcagta ccagtgccat gtcccagaca ggctcgcatc ccgggagggg 450		
cttggcaggg cgctggctgt ggggagccca accctgcctc ctgctcccc 500		
ttgtgccgt ctccctggctg gtgtggctgc ttctgctact gctggcctct 550		
ctcctgccct cagcccggtc ggccagcccc ctccccccggg aggaggagat 600		
cgtgtttcca gagaagctca acggcagcgt cctgcctggc tcgggcgcc 650		
ctgccaggct gttgtgccgc ttgcaggcct ttggggagac gctgctacta 700		
gagctggagc aggactccgg tgtgcaggtc gaggggctga cagtgcagta 750		
cctgggccag gcgcctgagc tgctgggtgg agcagagcct ggacacctacc 800		
tgactggcac catcaatgga gatccggagt cggtgtccatc tctgcactgg 850		
gatgggggag ccctgttagg cgtgttacaa tatcgaaaaa ctgaactcca 900		
cctccagccc ctggagggag gcacccctaa ctctgctggg ggacctgggg 950		

ctcacatcct acgcccgaag agtcctgcc a cggtcaagg tcccatgtgc 1000  
aacgtcaagg ctccctttgg aagccccagc cccagacccc gaagagccaa 1050  
gcgcttgct tcactgagta gatttgtga gacactggc gtggcagatg 1100  
acaagatggc cgcattccac ggtgcggggc taaagcgcta cctgctaaca 1150  
gtgatggcag cagcagccaa ggccttcaag caccaagca tccgcaatcc 1200  
tgtcagctt gttgtgactc ggctagtat cctggggtca ggcgaggagg 1250  
ggccccaagt gggcccaagt gctgcccaga ccctgcgcag cttctgtgcc 1300  
tggcagcggg gcctcaacac ccctgaggac tcggccctg accactttga 1350  
cacagccatt ctgtttaccc gtcaggaccc gtgtggagtc tccacttgcg 1400  
acacgctggg tatggctgat gtgggcaccg tctgtgaccc ggctcgagc 1450  
tgtgccattt tggaggatga tgggctccag tcagccttca ctgctgctca 1500  
tgaactgggt catgtcttca acatgctcca tgacaactcc aagccatgca 1550  
tcagttgaa tgggcctttg agcacctctc gccatgtcat ggccctgtg 1600  
atggctcatg tggatcctga ggagccctgg tccccctgca gtgcccgtt 1650  
catcaactgac ttccctggaca atggctatgg gcactgtctc ttagacaaac 1700  
cagaggctcc attgcattctg cctgtgactt tccctggcaa ggactatgat 1750  
gctgaccgccc agtgcacact gacccctggg cccgactcac gccattgtcc 1800  
acagctgccc cggccctgtg ctggcccttg gtgctctggc cacctcaatg 1850  
gccatgccat gtgccagacc aaacactcgc cctggccga tggcacaccc 1900  
tgcgggccccg cacaggcctg catgggtggt cgctgcctcc acatggacca 1950  
gctccaggac ttcaatattc cacaggctgg tggctgggt ccttgggac 2000  
catgggtga ctgctctcgg acctgtgggg gtgggtgtcca gttctcctcc 2050  
cgagactgca cgaggcctgt ccccccgaat ggtggcaagt actgtgaggg 2100  
ccggccgtacc cgcttccgct cctgcaacac tgaggactgc ccaactggct 2150  
cagccctgac cttccgcgag gagcagtgtg ctgcctacaa ccaccgcacc 2200  
gacctttca agagcttccc agggcccatg gactgggttc ctcgctacac 2250  
aggcgtggcc ccccaggacc agtgcaaact cacctgccag gcccggcacc 2300  
tgggctacta ctatgtgctg gagccacggg tggtagatgg gacccctgt 2350  
tccccggaca gctcctcggt ctgtgtccag ggccgatgca tccatgctgg 2400

ctgtgatcgc atcattggct ccaagaagaa gtttgacaag tgcatagggt 2450  
gcggaggggga cggttctggc tgccagcaagc agtcaggctc cttcaggaaa 2500  
ttcaggtacg gataacaacaa tgtggtact atcccccgcc gggccaccca 2550  
cattcttgtc cggcagcagg gaaaccctgg ccaccggagc atctacttgg 2600  
ccctgaagct gccagatggc tcctatgccc tcaatggtga atacacgctg 2650  
atgccctccc ccacagatgt ggtactgcct ggggcagtca gcttgcgcta 2700  
cagcggggcc actgcagcct cagagacact gtcaggccat gggccactgg 2750  
cccagccctt gacactgcaa gtcccttagtgg ctggcaaccc ccaggacaca 2800  
cgccctccgat acagcttctt cgtccccgg ccgaccctt caacgcccacg 2850  
ccccactccc caggactggc tgcaccgaag agcacagatt ctggagatcc 2900  
ttcggcggcg cccctggcg ggcaggaaat aacctcacta tcccggtgc 2950  
cctttctggg caccggggcc tcggacttag ctgggagaaa gagagagctt 3000  
ctgttgctgc ctcatgctaa gactcagtgg ggagggctg tggcgtgag 3050  
acctgcccct cctctctgcc ctaatgcgcga ggctggccct gccctgggtt 3100  
cctgcccctgg gaggcagtga tgggttagtg gatggaaggg gctgacagac 3150  
agccctccat ctaaactgcc ccctctgccc tgcgggtcac aggagggagg 3200  
gggaaggcag ggagggcctg ggccccagtt gtatttattt agtattttt 3250  
cacttttatt tagcaccagg gaaggggaca aggactaggg tcctgggaa 3300  
cctgaccctt gaccctcat accctcacc ctggggctag gaaatccagg 3350  
gtgggtgtga taggtataag tgggtgtgt atgcgtgtgt gtgtgtgtgt 3400  
gaaaatgtgt gtgtgcttat gtatgaggtt caacctgttc tgcttcctc 3450  
ttcctgaatt ttattttttggaaaagaaa agtcaagggt agggtgggccc 3500  
ttcagggagt gagggattat cttttttttt ttttcttctt ttctttcttt 3550  
tttttttttgg agacagaatc tcgctctgtc gcccaggctg gagtgcaatg 3600  
gcacaatctc ggctcactgc atccctccgcc tcccggttc aagtgattct 3650  
catgcctcag cctcctgagt agctgggatt acaggctcct gccaccacgc 3700  
ccagctaatt tttgttttgt tttgtttggaa gacagagtct cgctattgtc 3750  
accaggcgtg gaatgatttc agctcactgc aaccttcgcc acctgggttc 3800  
cagcaattct cctgcctcag cctcccgagt agctgagatt ataggcacct 3850

accaccacgc ccggcttaatt tttgtatTTT tagtagagac ggggtttcac 3900  
catgttggcc aggctggctc cgaactcctg accttaggtg atccactcgc 3950  
cttcatctcc caaagtgcgtg ggattacagg cgtgagccac cgtgcctggc 4000  
cacgcccAAC taatTTTGT attTTAGTA gagacAGGGT ttCACCATGT 4050  
tggccaggct gctcttgaac tcctgacctc aggtaatcga cctgcctcg 4100  
cctcccaaAG tgctgggatt acaggtgtga gccaccacgc ccggtaCATA 4150  
tttttaaAT tgaatttac tatttatgtg atcctttgg agtcagacag 4200  
atgtggTTGc atcctaactc catgtctctg agcattAGAT ttctcatttg 4250  
ccaataataa tacctccCTT agaagTTGT tgtgaggatt aaataatgta 4300  
aataaagaAC tagcataaca ctcaaaaaAA aaaaaaaaaA aaaaaaaaaA 4350  
aaaaaaaaAA aaaaaaaaaA aaaaaaaaaA aaaaaaaaaA aaaaaaaaaA 4400  
aaggAAA 4407

<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg
1				5				10					15	

Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro
				20				25					30	

Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	
				35				40				45		

Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
				50				55				60		

Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
				65				70				75		

Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
				80				85				90		

Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
				95				100				105		

Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
				110				115				120		

Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
				125				130				135		

Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Ala Leu Leu

140	145	150
Gly Val Leu Gln Tyr Arg Gly Ala Glu	Leu His Leu Gln Pro	Leu
155	160	165
Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His	Ile
170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys	Asn
185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg	Ala
200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val	Val
215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys	Arg
230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Ala Lys Ala Phe Lys	His
245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu	Val
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser	Ala
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu	Asn
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile	Leu
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr	Leu
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser	Cys
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala	Ala
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser	Lys
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His	Val
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp	Ser
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly	Tyr
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu	Pro
425	430	435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln  
440 445 450

Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro  
455 460 465

Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala  
470 475 480

Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys  
485 490 495

Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp  
500 505 510

Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro  
515 520 525

Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Val  
530 535 540

Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly  
545 550 555

Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn  
560 565 570

Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu  
575 580 585

Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe  
590 595 600

Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro  
605 610 615

Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr  
620 625 630

Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser  
635 640 645

Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala  
650 655 660

Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys  
665 670 675

Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly  
680 685 690

Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile  
695 700 705

Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro  
710 715 720

Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

	725		730		735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp					
	740		745		750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr					
	755		760		765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro					
	770		775		780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg					
	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro					
	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu					
	815		820		825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys					
	830		835		

<210> 318  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 318  
ccctgaagct gccagatggc tcc 23

<210> 319  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 319  
ctgtgctttt cggtgcagcc agtc 24

<210> 320  
<211> 43  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-43  
<223> Synthetic construct.

<400> 320  
ccacagatgt ggtactgcct gggcagtca gcttgcgcta cag 43

<210> 321  
<211> 1197  
<212> DNA  
<213> Homo sapiens

<400> 321  
cagcagtgg ctctcagtcc tctcaaagca aggaaagagt actgtgtgct 50  
gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100  
ctaaatgcag aagctttaa atccaagaaa atatgtaaat cacttaagat 150  
ttgtggactg gtgtttggta tcctggccct aactctaatt gtcctgttt 200  
gggggagcaa gcacttctgg ccggaggtac ccaaaaaaagc ctatgacatg 250  
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300  
tgatcctgtg accagaactg aaatattcag aagcgaaaat ggcactgatg 350  
aacatttggaa agtgcacogac tttaaaaacg gatacactgg catctacttc 400  
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450  
attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500  
ctttcttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550  
aaccgagatt ttctaaaaaa ttccaaaatt ctggagattt gtgataacgt 600  
gaccatgtat tggatcaatc ccactctaatt atcagtttct gagttacaag 650  
actttgagga ggagggagaa gatcttact ttccctgcaa cgaaaaaaaa 700  
gggattgaac aaaatgaaca gtgggtggc cctcaagtga aagtagagaa 750  
gaccgtcac gccagacaag caagtgagga agaacttcca ataaatgact 800  
atactgaaaa tggaaatagaa tttgatccc tgctggatga gagaggttat 850  
tgttgtatTTT actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900  
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950  
tcatctgtcg tgtcatcatg ccttctaact ggtgggtggc ccgcattgtg 1000  
gggagggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050  
atataataaa tgcatgctat tcaatgaatt tctgcctatg aggcattctgg 1100  
ccccctggtag ccagctctcc agaattactt gtaggttaatt cctctttca 1150  
tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaaa 1197

<210> 322

<211> 317  
<212> PRT  
<213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	
1		5				10							15		
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
		20					25						30		
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
		35					40						45		
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
		50						55					60		
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
		65						70					75		
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
		80						85					90		
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
		95						100					105		
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
		110						115					120		
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
		125						130					135		
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
		140						145					150		
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
		155						160					165		
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
		170						175					180		
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
		185						190					195		
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
		200						205					210		
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
		215						220					225		
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
		230						235					240		
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
		245						250					255		
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
		260						265					270		

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly  
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys  
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly  
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

gcggaactgg ctccggctgg cacctgagga gcggcggtac cccgagggcc 50

cagggagctg cccggctggc ctaggcaggc agccgcacca tggccagcac 100

ggccgtgcag cttctggct tcctgctcag cttcctggc atgggtggca 150

cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtggc 200

accaacatcc tcacggccgt gtccctacctg aaagggtctt ggatggagt 250

tgtgtggcac agcacaggca tctaccatgt ccagatctac cgatccctgc 300

tggcgctgcc ccaagacctc caggctgcc ggcgcctcat ggtcatctcc 350

tgcctgctct cgggcatacg ctgcgcctgc gccgtcatcg ggatgaagt 400

cacgcgtgc gccaaggggca cacccgccaa gaccacctt gccatcctcg 450

gcggcaccct cttcatcctg gccggcctcc tgtgcattgtt ggccgtctcc 500

tggaccacca acgacgttgtt gcagaacttc tacaacccgc tgctgcccag 550

cggcatgaag tttgagattt gcccaggccct gtacccgttgc ttcatctcct 600

cgtccctctc gtcatttgtt ggccacctgc tttgcctgtc ctgccaggac 650

gaggcaccctt acaggcccta ccaggccccg cccagggcca ccacgaccac 700

tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750

gggccccctc agtgacccctcg gccacgcaca gcgggtacag gctgaacgac 800

tacgtgtgag tccccacagc ctgcattctcc cctggctgc tgtggctgg 850

gtccccggcg ggactgtcaa tggaggcagg ggttccagca caaagttac 900

ttctggccaa ttttgtatc caaggaaata atgtgaatgc gagaaatgt 950

ctttagagca cagggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaaaaa aaatcctgtc tgttttgtat tttattatat 1050  
atatttatgt gggtgatttg ataacaagtt taatataaag tgacttggga 1100  
gttggtcag tggggttgggt ttgtgatcca ggaataaacc ttgcggatgt 1150  
ggctgtttat gaaaaaaaaaaa aaaa 1174

<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
1					5				10				15	
Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp
			20					25				30		
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser
				35				40				45		
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly
				50				55			60			
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65				70			75			
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu
				80				85			90			
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr
				95				100			105			
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu
				110				115			120			
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala
				125				130			135			
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro
				140				145			150			
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr
				155				160			165			
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu
				170				175			180			
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln
				185				190			195			
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	
				200				205			210			
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val
				215				220			225			

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val  
230 235

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

gagctccct caggagcgcg ttagcttcac accttcggca gcaggaggc 50

ggcagttct cgccaggcggc agggcggcg gccaggatca tgtccaccac 100

cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150

gcatcgccgc caccggatg gacatgtgga gcacccagga cctgtacgac 200

aaccccgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250

gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300

gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350

gtcctgggtg ccattggcct cctggtatcc atcttgccc taaaatgcat 400

ccgcattggc agcatggagg actctgccaa agccaacatg acactgacct 450

ccgggatcat gttcattgtc tcaggtctt gtgcaattgc tggagtgtct 500

gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550

gtacaccggc atgggtggga tggcgcagac tggtcagacc aggtacacat 600

ttggcgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650

gggggtgtga tggatgtgc tgcctggcgg ggcctggcac cagaagaaac 700

caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750

agcctggagg cttcaaggcc agcaactggct ttgggtccaa cacaaaaaac 800

aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatctta 850

tccttccaag cacgactatg tgtaatgctc taagacctct cagcacggc 900

ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950

atttcttctt gctttgact cacagctgga agttagaaaa gcctcgattt 1000

catctttgga gaggccaaat ggtcttagcc tcagtcgtc tctctaaata 1050

ttccaccata aaacagctga gttatattatg aatttagaggc tatagctcac 1100

attttcaatc ctctatttct ttttttaaat ataactttct actctgatga 1150

gagaatgtgg tttaatctc tctctcacat tttgatgatt tagacagact 1200

ccccctcttc ctcctagtc ataaacccat tgatgatcta tttcccagct 1250

tatccccaaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300  
ttctgctgtt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350  
cacttactga agaagaagca ataagagaaa gatatttgc atctctccag 1400  
cccatgatct cggttttctt acactgtgat cttaaaagtt accaaaccaa 1450  
agtcatttc agtttgggc aaccaaacct ttctactgct gttgacatct 1500  
tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550  
tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600  
atttttttta atttaagtcc taaatatagt taaaataaaat aatgttttag 1650  
taaaatgata cactatctct gtgaaatagc ctcaccccta catgtggata 1700  
gaaggaaatg aaaaaataat tgcttgaca ttgtctatat ggtactttgt 1750  
aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800  
agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850  
gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900  
aaaaaatcag ccagtcatgg tggcatacac ctgttagtccc agcattccgg 1950  
gaggctgagg tgggaggatc acttgagccc agggaggttg gggctgcagt 2000  
gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
gtctaaaaaaaaataatggaa cacagcaagt cctaggaagt 2100  
aggttaaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
1														15

Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
						20			25					30

Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
										35				45

Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
									50					60

Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
									65					75

Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg		
95	100	105
Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr		
110	115	120
Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly		
125	130	135
Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser		
140	145	150
Thr Ala Asn Met Tyr Thr Gly Met Gly Gly Met Val Gln Thr Val		
155	160	165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val		
170	175	180
Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala		
185	190	• 195
Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser		
200	205	210
Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe		
215	220	225
Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile		
230	235	240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro		
245	250	255
Ser Lys His Asp Tyr Val		
260		
<210> 327		
<211> 2010		
<212> DNA		
<213> Homo sapiens		
<400> 327		
ggaaaaactg ttctttctg tggcacagag aaccctgctt caaaggcaga 50		
gtacgttc cggagtccag ctggctaaaa ctcatcccag aggataatgg 100		
caacccatgc cttagaaatc gctggctgt ttcttggtgg tggtaatg 150		
gtggcacag tggctgtcac tgtcatgcct cagtggagag tgccggcctt 200		
cattgaaaac aacatcgtagg ttttgaaaa cttctggaa ggactgtgga 250		
tgaattgcgt gaggcaggct aacatcgtagg tgccgtgcaa aatctatgtat 300		
tccctgctgg ctctttctcc ggacctacag gcagccagag gactgtgtg 350		

tgctgcttcc gtgatgtcct tcttggctt catgtggcc atcctggca 400  
tgaaatgcac caggtgcacg ggggacaatg agaaggtaa ggctcacatt 450  
ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tggtgctcat 500  
ccctgtgagc tgggttgcct atgccatcat cagagattc tataactcaa 550  
tagtgaatgt tgcccaaaaa cgtgagctg gagaagctct ctacttagga 600  
tggaccacgg cactggtgct gattgttgg a gagctctgt tctgctgcgt 650  
tttttgtgc aacgaaaaga gcagtagcta cagatactcg atacccccc 700  
atcgacaaac ccaaaaaagt tatcacaccc gaaagaagtc accgagcgtc 750  
tactccagaa gtcagttatgt gtagttgtgt atgtttttt aactttacta 800  
taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc 850  
caaagaaact ttgatttact gttcttaact gcctaattttt aattacagga 900  
actgtgcac agctatttat gattctataa gctatttcag cagaatgaga 950  
tattaaaccc aatgctttga ttgttctaga aagtatagta atttggtttc 1000  
taaggtggtt caagcatcta ctcttttat catttacttc aaaatgacat 1050  
tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100  
tatgtacata gatgagtgta acatttat ctcacataga gacatgctta 1150  
tatggttta tttaaaatga aatgccagtc cattacactg aataaataga 1200  
actcaactat tgcttttcag gaaatcatg gatagggttt aagaaggta 1250  
ctattaattt tttaaaaca gcttagggat taatgtcctc catttataat 1300  
gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350  
tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400  
atccctttct cccagaggct tttttttct tgtgtattaa attaacattt 1450  
ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgctttcc 1500  
agggtataac tcagaagaaa gataaaagtg tgatctaaga aaaagtgtatg 1550  
gttttaggaa agtggaaata tttttgtttt tgtatggaa gaagaatgat 1600  
gcattttgac aagaaatcat atatgtatgg atatatttttta ataagtattt 1650  
gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata 1700  
tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750  
ccttgagaa ctccacactgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgttag 1850  
tttactaaa atctgtaaat actgtatTTT tctgtttatt ccaaatttga 1900  
tgaaactgac aatccaattt gaaagtttgt gtgcacgtct gtctagctta 1950  
aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000  
ttttctaatt 2010

<210> 328  
<211> 225  
<212> PRT  
<213> Homo sapiens

<400> 328  
Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly  
1 5 10 15  
Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp  
20 25 30  
Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn  
35 40 45  
Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile  
50 55 60  
Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro  
65 70 75  
Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met  
80 85 90  
Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr  
95 100 105  
Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu  
110 115 120  
Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile  
125 130 135  
Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn  
140 145 150  
Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu  
155 160 165  
Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala  
170 175 180  
Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr  
185 190 195  
Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His  
200 205 210

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val  
215 220 225

<210> 329

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

tcggccatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50  
ctgggctggg tgaatggcct ggtctcctgt gccctgccc tgtggaagg 100  
gaccgcttc atcggcaaca gcacgtggt ggcccaggtg gtgtgggagg 150  
gcctgtggat gtcctgcgtg gtgcagagca ccggccagat gcagtgc 200  
gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250  
cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300  
ttgtctgggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350  
cgccctggtgc tcacctctgg gattgtcttt gtcatctcag gggcctgac 400  
gctaatacccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450  
accccccgtt ggctgaggcc caaaagcggg agctggggc ctccctctac 500  
ttgggctggg cggcctcagg cctttgttg ctgggtgggg gtttgcgtg 550  
ctgcacttgc ccctcgaaaa ggtcccaggcc cccagccat tacatggccc 600  
gctactcaac atctgcccct gccatctc gggggccctc tgagtaccct 650  
accaagaatt acgtctgacg tggagggaa tgggggctcc gctggcgcta 700  
gagccatcca gaagtggcag tgcccaacag ctttggatg gttcgttacc 750  
ttttgtttct gcctcctgct attttcttt tgactgagga tatttaaat 800  
tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850  
gctgtttctc acccttggat gatggagccaa aagagggat gctttgagat 900  
tctggatctt gacatgcccc tcttagaagc cagtcaagct atgaaactaa 950  
tgcggaggct gcttgctgtg ctggcttgc aacaagacag actgtcccc 1000  
agagttcctg ctgctgtgg gggctggct tccctagatg tcactggaca 1050  
gctgcccccc atcctactca ggtctctgga gtcctctct tcacccctgg 1100  
aaaaacaaat catctgttaa caaaggactg cccacctccg gaacctctga 1150  
cctctgtttc ctccgtcctg ataagacgtc cacccccccag ggccaggtcc 1200  
cagctatgtaa gaccccccggcc cccacctccaa acactgcacc cttctggccct 1250

gccccccctcg tctcacccccc tttacactca catttttatac aaataaaagca 1300  
tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu  
1 5 10 15

Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp  
20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val  
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly  
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln  
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val  
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr  
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr  
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro  
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro  
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr  
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Gly Gly Gly Leu  
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His  
185 190 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly  
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val  
215 220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

gcacaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50  
ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100  
gtaaaaggcaa tggcatttta tcccttgcaa attgctggc tggttcttgg 150  
gttccttggc atggtgggaa ctttgccac aacccttctg cctcagtgg 200  
ggagtatcag ctttgttgg cagcaacatt attgtcttgg agaggctctg 250  
ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300  
gcaagttcta tagctccttgc ttggctctcc cgccctgcctt gaaaaacagcc 350  
cgggccctca tgtgtgtggc tggctctc tccttgcata cgctgcttat 400  
tggcatctgt ggcataaagc aggtccagtg cacaggctct aacgagaggg 450  
ccaaagcata cttctggaa acttcaggag tcctcttcat cctgacgggt 500  
atcttcgttc tgattccggg gagctggaca gccaatataa tcatcagaga 550  
tttctacaac ccagccatcc acataggtaa gaaacgagag ctgggagcag 600  
caactttcct tggctggca agcgctgctg tcctcttcat tggaggggt 650  
ctgctttgtg gatTTTGTG ctgcaacaga aagaagcaag ggtacagata 700  
tccagtgccc ggctaccgtg tgccacacac agataagcga agaaatacga 750  
caatgtttag taagacctcc accagttatg tctaattgcct cttttggct 800  
ccaagtatgg actatggta atgttttta taaagtccctg ctagaaactg 850  
taagtatgtg aggcaaggaga acttgcttta tgtcttagatt tacattgata 900  
cgaaagtttc aatttgttac tggggtagg aatgaaaatg acttacttgg 950  
acattctgac ttcaggtgta ttaaatgcattt tgactattgt tggacccat 1000  
cgctgctcca attttcatat tctaaattca agtataccca taatcatttag 1050  
caagtgtaca atgatggact acttattact tttgaccat catgtattat 1100  
ctgataagaa tctaaagttt aaattgatatt tctataacaa taaaacatat 1150  
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg			
20	25		30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu			
35	40		45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn			
50	55		60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe			
65	70		75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala			
80	85		90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly			
95	100		105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser			
110	115		120
Ala Ala Val Leu Phe Ile Gly Gly Leu Leu Cys Gly Phe Cys			
125	130		135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly			
140	145		150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu			
155	160		165
Ser Lys Thr Ser Thr Ser Tyr Val			
170			

<210> 333  
<211> 535  
<212> DNA  
<213> Homo sapiens

<400> 333  
agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50  
atcactgggg gtctccttct gctctgtaca gtggtctatt tctgttagcag 100  
ctcagaagct gctagtcgt ctccaaaaaa agtggactgc agcatttaca 150  
agaagtatcc agtggtggcc atcccctgcc ccatcacata cctaccagtt 200  
tgtggttctg actacatcac ctatggaat gaatgtcaact tgtgtaccga 250  
gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300  
aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350  
tcatcatccc aggctctgac tgagttctt tcagtttac tgatgttctg 400  
ggtgaaaaac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcatttt 500  
ttttaaacac gtcaataaaa aaataatctc ccaga 535

<210> 334  
<211> 85  
<212> PRT  
<213> Homo sapiens

<400> 334  
Met Lys Ile Thr Gly Gly Leu Leu Leu Cys Thr Val Val Tyr  
1 5 10 15  
Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val  
20 25 30  
Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
35 40 45  
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
50 55 60  
Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
65 70 75  
Arg Val Gln Phe Leu His Asp Gly Ser Cys  
80 85

<210> 335  
<211> 742  
<212> DNA  
<213> Homo sapiens

<400> 335  
cccgccccc gtttccctc gcagcacctc gaagtgcgcc cctcgccctc 50  
ctgctcgcc cccgccccca tggctgcctc ccccgccgg cctgctgtcc 100  
tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccagg 150  
ggcataagtg gaaataaact caagctgatg cttaaaaac gagaagcacc 200  
tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250  
tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300  
cccgagggtgc agcagtggtt ccagcagttt ctctacatgg gctttgatga 350  
agcgaaattt gaagatgaca tcacctattt gcttaacaga gatcgaaatg 400  
gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450  
gcaattggtc cccggagccc ctacggcttt aggcatggag ccagcgtcaa 500  
ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550  
agcgattctc ttcatgtatc tcctaatgcc ttacactact tggttctga 600

tttgcttat ttcagcagat ctttctacc tactttgtgt gatcaaaaaa 650  
gaagagttaa aacaacacat gttaatgcct tttgatattt catggaaatg 700  
cctctcattt aaaaatagaa ataaaggcatt ttgttaaaaa ga 742

<210> 336  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 336  
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly  
1 5 10 15  
Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser  
20 25 30  
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val  
35 40 45  
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
50 55 60  
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
65 70 75  
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
80 85 90  
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
95 100 105  
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
110 115 120  
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr  
125 130 135  
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr  
140 145

<210> 337  
<211> 1310  
<212> DNA  
<213> Homo sapiens

<400> 337  
cggtcgagc ccgccccgaa gtgcccggagg ggccgcgatg gagctgggg 50  
agccgggcgc tcggtagcgc ggcggcaag gcaggcgcca tgaccctgat 100  
tgaagggtg ggtgatgagg tgaccgtct tttctcggtg cttgcctgcc 150  
ttctgggtct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcg 200  
gaccactgc cccagccgtc agggacccc acgccatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccc gggcagaga 300  
cccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacg 350  
gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcg 400  
gctacggctg aaattcctca atgattcaga gcaggtggcc agggcctggc 450  
cccacgacac cattggctcc ttgaaaagga cccagttcc cggccggaa 500  
cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacaccca 550  
gaccctgggc agccttacc tccctccaa ctgcgttctc cactgccacg 600  
tgtccacgag agtcggtccc ccaaattcccc cctgcccggc ggggtccgag 650  
cccgccccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700  
cctgctgttg ctgctgctct ggtactgcc aatccagttac cggcccttct 750  
ttccctgac cgccactctg ggctggccg gtttcaccct gtcctcagt 800  
ctcctggcct ttgccatgta cggcccttag tgccctcccg ggcgttggc 850  
agcgtcggc gcccctccgg accttgcctcc cgcgcggcgc gggggagctg 900  
ctgcctgccc aggccccct ctccggcctg cctttcccg ctgcctgga 950  
gcccagccct gcgcgcaga ggactccgg gactggcgga ggccccggcc 1000  
tgcgaccgcc ggggctcgcc gccacccccc ggggctgctg aacctcagcc 1050  
cgcaactggga gtgggctccct cggggctcgcc catctgctgt cgctgcctcg 1100  
gccccggca gagccgggcc gccccgggg cccgtcttag tggtctgccg 1150  
gaggacccag ccgcctccaa tccctgacag ctccctggc tgagttgggg 1200  
acgccaggc ggtgggaggc tggtaaggg gagcggggag gggcagagga 1250  
gttccccgga acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaaa 1300  
aaaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
1				5					10				15	

Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25				30	

Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35				40				45		

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp
					50					55				60
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg
					65					70				75
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr
					80					85				90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu
					95					100				105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp
					110					115				120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly
					125					130				135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly
					140					145				150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys
					155					160				165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro
					170					175				180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile
					185					190				195
Gly	Ser	Leu	Leu	Leu	Pro	Leu								
					200					205				210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala
					215					220				225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala
					230					235				240
Phe	Ala	Met	Tyr	Arg	Pro									
					245									

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

gagattggaa acagccaggt tggaggcagt agtgagtaag gaaacctggc 50

tgcctctcc agattccccca ggctctcaga gaagatcagc agaaaagtctg 100

caagacccta agaaccatca gccctcagct gcaccccttc ccctccaagg 150

atgacaaagg cgctactcat ctatggtc agcagtttc ttgccctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcggcagggtg ctgcagctgg 250

aggacttgga tgggttgag gtttactccc tgagtgactg gctgtgcctg 300  
gctttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350  
tggaagcttt gactatggcc tcttcagat caacagccac tactggtgca 400  
acgattataa gagttactcg gaaaacctt gccacgtaga ctgtcaagat 450  
ctgctgaatc ccaaccctct tcgcaggcatc cactgcgcaa aaaggattgt 500  
gtccggagca cggggatga acaactgggt agaatggagg ttgcactgtt 550  
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600  
agggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650  
ggattcttca tttcttcctc ctactgcctc cacttcatgt tattttcttc 700  
ccttcccatt tacaactaaa actgaccaga gccccagggaa taaatggttt 750  
tcttgcttc ctccctactc ccacatggac ccagtccttc ggttcctgtc 800  
tgttatttgtt aaactgagga ccacaataaa gaaatctta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala  
1 5 10 15

Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val  
20 25 30

Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser  
35 40 45

Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser  
50 55 60

Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe  
65 70 75

Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser  
80 85 90

Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn  
95 100 105

Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala  
110 115 120

Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly  
125 130 135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341  
<211> 23  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.  
  
<400> 341  
ccctccaagg atgacaaagg cgc 23

<210> 342  
<211> 29  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-29  
<223> Synthetic construct.  
  
<400> 342  
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343  
<211> 24  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.  
  
<400> 343  
atctcaggcg gcattctgttc agcc 24

<210> 344  
<211> 24  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 344  
gtggatgcct gcaagaaggt tggg 24  
  
<210> 345  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 345  
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346  
<211> 2575  
<212> DNA  
<213> Homo sapiens

<400> 346  
tctgaccta ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50  
actgagaacc caccagctca tcccagacac ctcatalogcaa cctatttata 100  
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150  
aaggagaaaa ccggggtaaa gggagggaaag caattcaatt tgaagtccct 200  
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250  
ggggtgaaac ttgggtcctg tggtttctg attgttaagtg gaagcaggc 300  
ttgcacacgc ttttggcaaa tgtcaggacc aggttaagtg actggcagaa 350  
aaacttccag gtggacaag caacccatgt tctgctgcaa gcttgaagga 400  
gcctggagcg ggagaaagct aacttgaaca tgacctgtt catttggcaa 450  
gttctagcaa catgctcccta aggaagcgtt acaggcacag accatgcaga 500  
ctccagttcc tcctgctgct cctgatgctg ggatgcgtcc tcatgtatgg 550  
ggcgatgtt caccctcccc accacaccct gcaccagact gtcacagccc 600  
aagccagcaa gcacagccct gaagccaggt accgccttga ctttgggaa 650  
tcccaggatt gggtaacttga agctgaggat gagggtgaag agtacagccc 700  
tctggagggc ctgccacccct ttatctcaact gcgggaggat cagctgctgg 750  
tggccgtggc cttacccctt gccaagaagga accagagcca gggcaggaga 800  
ggtgtggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850  
cccaaagagg gactgggggg ctgatgagga cggggaggtg tctgaagaag 900  
aggagttgac cccgttcagc ctggacccac gtggcctcca ggaggcactc 950  
agtgcggca tccccctcca gagggctctg cccgaggtgc ggcacccact 1000  
gtgtctgcag cagcaccctc aggacagcct gcccacagcc agcgtcatcc 1050  
tctgtttcca tcatgaggcc tggtccactc tcctgcggac tgtacacagc 1100

atcctcgaca cagtccccag ggccttcctg aaggagatca tcctcggtgg 1150  
cgacccctcagc cagcaaggac aactcaagtc tgctctcagc gaatatgtgg 1200  
ccaggctgga gggggtaaag ttactcagga gcaacaagag gctgggtgcc 1250  
atcaggccc ggatgctggg ggccaccaga gccaccgggg atgtgctcgt 1300  
tttcatggat gcccactgcg agtgccaccc aggctggctg gagcccctcc 1350  
tcagcagaat agctggtgac aggagccgag tggtatctcc ggtgatagat 1400  
gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450  
tgggtgttg gactggaagc tggatttcca ctggaaacct ttgccagagc 1500  
atgtgaggaa ggccctccag tccccataa gccccatcag gagccctgtg 1550  
gtgcccggag aggtggtggc catggacaga cattactcc aaaacactgg 1600  
agcgtatgac tctcttatgt cgctgcgagg tggtaaaac ctcgaactgt 1650  
cttcaaggc ctggctctgt ggtggctctg ttgaaatcct tccctgctct 1700  
cggttaggac acatctacca aaatcaggat tcccatccc ccctcgacca 1750  
ggagggccacc ctgaggaaca gggttcgcat tgctgagacc tggctgggt 1800  
cattcaaaga aacttctac aagcatagcc cagaggcctt ctccctgagc 1850  
aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900  
gggttgcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950  
accatctga acccaggccc agtttctctg gaaagctcca caacactgg 2000  
cttggctct gtgcagactg ccaggcagaa gggacatcc tggctgtcc 2050  
catggtgttgc gtccttgca gtgacagccg gcagcaacag tacctgcagc 2100  
acaccagcag gaaggagatt cactttggca gcccacagca cctgtgcttt 2150  
gctgtcaggc aggagcaggt gatttttcag aactgcacgg aggaaggcct 2200  
ggccatccac cagcagcaact gggacttcca ggagaatggg atgattgtcc 2250  
acattcttc tggaaatgc atgaaagctg tggtgcaaga aaacaataaa 2300  
gatttgtacc tgcgtccgtg tggatggaaaa gcccggccagc agtggcgatt 2350  
tgaccagata aatgctgtgg atgaacgatg aatgtcaatg tcagaaggaa 2400  
aagagaattt tggccatcaa aatccagctc caagtgaacg taaaagagctt 2450  
atatatttca tgaagctgat cttttgtgt gtgtgctcct tggtagga 2500  
gagaaaaaaag ctctatgaaa gaatataggaa agtttctcct tttcacacacct 2550

tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln  
1 5 10 15

Phe Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val  
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr  
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp  
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly  
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu  
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg  
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Ser Tyr Arg Leu Ile  
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp  
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr  
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala  
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu  
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val  
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr  
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu  
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser  
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu  
245 250 255

Arg Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly  
 260 265 270  
 Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His  
 275 280 285  
 Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile  
 290 295 300  
 Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile  
 305 310 315  
 Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg  
 320 325 330  
 Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro  
 335 340 345  
 Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg  
 350 355 360  
 Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr  
 365 370 375  
 Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly  
 380 385 390  
 Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly  
 395 400 405  
 Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln  
 410 415 420  
 Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg  
 425 430 435  
 Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu  
 440 445 450  
 Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala  
 455 460 465  
 Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu  
 470 475 480  
 Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu  
 485 490 495  
 Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His  
 500 505 510  
 Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp  
 515 520 525  
 Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg  
 530 535 540  
 Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe

545                    550                    555  
Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val  
560                    565                    570  
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln  
575                    580                    585  
His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser  
590                    595                    600  
Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu  
605                    610                    615  
Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe  
620                    625                    630  
Asp Gln Ile Asn Ala Val Asp Glu Arg  
635

<210> 348  
<211> 23  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.  
  
<400> 348  
ggagaggtgg tggccatgga cag 23  
  
<210> 349  
<211> 24  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.  
  
<400> 349  
ctgtcactgc aaggagccaa cacc 24  
  
<210> 350  
<211> 45  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.  
  
<400> 350  
tatgtcgctg cgaggtggtg aaaacctcga actgtcttc aaggc 45

<210> 351  
<211> 2524  
<212> DNA  
<213> Homo sapiens

<400> 351  
cgccaagcat gcagtaaagg ctgaaaatct gggcacacgc ttaggaagac 50  
ctcagacatg gagtccagga tgtggctgc gctgctgctg tcccacacctc 100  
tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150  
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccggtgtgc 200  
caggggaggc ccctcgcccc cacgtcatgt gtgcgtgtgg gagcgagcac 250  
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtccctg 300  
cctggcactg caccggcagc caccggatca ggcttgagg agggccgccc 350  
ctcatcccaa tacccctggg ctatcggtg gggtcccacc gtgtctcgag 400  
aggatggagg ggaccccaac tctgccaatc ccggatttct ggactatgg 450  
tttgcagccc ctcatgggct cgcaacccca caccggact cagactccat 500  
gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550  
ggccattcct gttcgggggc cgtggggaaag gtgtggaccc ccagctctat 600  
gtcacaatta ccatctccat catcattgtt ctctggcca ctggcatcat 650  
cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700  
agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750  
tccccggctg gagtcactgt gctggggcc ttctgggact caccctacccc 800  
caccctgac catgaggagc cccgaggggg accccggcct gggatgcccc 850  
accccaaggg ggctccagcc ttccagttga accgggtgagg gcaggggcaa 900  
tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950  
tgggggtgcc ctctggatgg gtagtgagga ggcaggcgtg gcctcccaca 1000  
gccccctggcc ctcccaaggg ggctggacca gtcctctct gggaggcacc 1050  
cttccttctc ccagtccttc aggatctgtg tcctattctc tgctgcccatt 1100  
aactccaact ctgcctctt tggtttttc tcatgccacc ttgtctaaga 1150  
caactctgcc ctcttaacct tgattcccc tctttgtctt gaacttcccc 1200  
ttctattctg gcctaccct tggttcctga ctgtgccctt tccctttcc 1250  
tctcaggatt cccctggtga atctgtgatg ccccaatgt tgggggtgcag 1300

ccaaggcagga ggccaaagggg ccggcacagc ccccatccca ctgagggtgg 1350  
ggcagctgtg gggagctggg gccacagggg ctcctggctc ctgcccctt 1400  
cacaccaccc ggaacactcc ccagccccac gggcaatcct atctgctcgc 1450  
cctcctgcag gtggggccct cacatatctg tgacttcggg tccctgtccc 1500  
cacccttgtg cactcacatg aaagcattgc acactcacct ccacccac 1550  
aggccatttg cacacgctcc tgccaccctct ccccgatccat accgctccgc 1600  
tcagctgact ctcatgttct ctcgtctcac atttgcactc tctccttccc 1650  
acattctgtg ctcagctcac tcagtggtca gcgtttcctg cacactttac 1700  
ctctcatgtg cgtttcccg cctgatgttg tggtggtgtg cggcgtgctc 1750  
actctctccc tcatgaacac ccacccaccc cgtttccgca gcccctgcgt 1800  
gctgctccag aggtgggtgg gaggtgagct gggggctccct tggggccctca 1850  
tcggtcatgg tctcgtccca ttccacacca tttgtttctc tgtctcccc 1900  
tcctactcca aggatgccgg catcaccctg agggctcccc cttggaaatg 1950  
gggttagtgag gccccagact tcaccccccag cccactgcta aaatctgtt 2000  
tctgacagat gggttttggg gagtcgcctg ctgcactaca tgagaaagg 2050  
actcccattt gcccctccct ttctcctaca gtcccttttgc tcttgcgt 2100  
cctggctgtc tgtgtgtgtg ccattctctg gacttcagag ccccctgagc 2150  
cagtcctccc ttcccagccct ccctttggc ctccttaact ccacctaggc 2200  
tgccagggac cggagtcaagc tggttcaagg ccatcgggag ctctgcctcc 2250  
aagtctaccc ttcccttccc ggactccctc ctgtcccctc cttcctccc 2300  
tccttccttc cacttcctt cctttgcctt ccctgcctt tcccccctt 2350  
caggttcttc ctccttctc actggttttt ccaccttccct cttcccttc 2400  
ttccctggct cctaggctgt gatataattttt tttgtattat ctcttc 2450  
ttcttggtt gatcatctt aattactgtg ggatgttaatg ttcaaaaattt 2500  
tcaaataaaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Lle	Arg	Gly
1					5				10				15	

Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	
								20		25			30	
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg
								35		40			45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala
								50		55			60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro
								65		70			75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys
								80		85			90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn
								95		100			105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu
								110		115			120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser
								125		130			135	
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg
								140		145			150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu
								155		160			165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln
								170		175			180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser
								185		190			195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp
								200		205			210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp
								215		220			225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu
								230		235			240	
Leu	Pro	Lys												

<210> 353  
<211> 480  
<212> DNA  
<213> Homo sapiens

<400> 353  
gttaaccaggc gcagtcctcc gtgcgtcccc cccgccgctg ccctcactcc 50  
cggccaggat ggcatcctgt ctggccctgc gcatggcgct gctgctggtc 100

tccgggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150  
cgtccccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
ccgtggagag caccagcccc ggccgggagc ccgtggacac cggtccccca 250  
gccccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
ggaccagggc ggcgggtcgc tggggcccg 350  
tcgcccct gctggccacc tgcgtggtgc tggcgctcg 400  
ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc ggcggccggcc 450  
gcggcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser	
1				5					10					15	
Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu	
		20					25						30		
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly	
			35					40					45		
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp	
			50				55						60		
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser	
			65				70						75		
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro	
			80				85						90		
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys	
			95					100					105		
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala	
			110					115					120		

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

ggccgttgt tggtgcgcgg ctgaagggtg tggcgcgagc agcgtcggt 50

gttggccggc ggccggccgg gacgggcattt gccctgtgc tgtgccttgt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150  
tctccaagaa gtttccttc taccgccacc atgtgaactt caagtccctgg 200  
tgggtggcgc acatccccgt gtcagggcgc ctgctcacccg actggagcga 250  
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300  
agaagctgga ccaagtggcgc acagcagtgt accagatgat ggatcagctg 350  
taccagggga agatgtactt ccccggttat ttccccaaacg agctgcgaaa 400  
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450  
acctggcacc aggcaagctgg ggaggaggc agctctccag ggagggaccc 500  
agcctagcac ctgaaggatc aatgccatca ccccgccccg acctccccta 550  
agtagcccc agaggcgctg ggagtgttgc caccgcctc ccctgaagtt 600  
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggcc 650  
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700  
tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750  
acgtcgccctg ctttggctat aactgcgagt agggctcagg catcacaccc 800  
accctgtCCA gggccctact gtccctgggg tcccaggctc tccttgagg 850  
gggctccccg ctttccacct ggctgtcatc gggtagggcgc gggccgtggg 900  
ttcagggcgc caccacttcc aagcctgtgt cccacaggctc ctggcgcag 950  
tggaaagtcaag ctgtccaggg cctcctgaac tacataaata actggcacaa 1000  
gtaaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050  
cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgta 1100  
ctagaggggc tcccggaggag gtggAACCTC aaccctaggctc tgccgcaggag 1150  
gcggctgcag tcctttctc cctcaaagggt ctccgaccct cagctggagg 1200  
cgggcatttt tcctaaagggt tcccatagg gtctgggttcc accccatccc 1250  
aggctgtgg tcagagcctg ggagggttcc ctacgatggt taggggtgcc 1300  
ccatggaggg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350  
tgaggtaagg ccggccctgac ctggacttca gggggaggggg gtaaaggag 1400  
agaggagggg ggcttaggggg tcctctagat cagtgggggc actgcaggtg 1450  
gggctctccc tatacctggg acacctgctg gatgtcacct ctgcaaccac 1500  
acccatgtgg tggtttcatg aacagaccac gtcctctgc cttctcctgg 1550

cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600  
ggcctcgga gaagggtgc tcgtaagcca acaccagcgt gccgcggcct 1650  
gcacaccctt cggacatccc aggacacgagg gtgtcggtga tgtggccaca 1700  
cataggacca cacgtcccag ctgggaggag aggcctgggg cccccaggga 1750  
gggaggcagg gggtgtgggga catggagagc tgaggcagcc tcgtctcccc 1800  
gcagcctggt atcgccagcc ttaaggtgtc tggagcccc acacttggcc 1850  
aacctgacct tggaaagatgc tgctgagtgt ctcaagcagc actgacagca 1900  
gctgggcctg ccccaggca acgtggggc ggagactcag ctggacagcc 1950  
cctgcctgtc actctggagc tggctgctg ctgcctcagg accccctctc 2000  
cgaccccgga cagagctgag ctggccaggg ccaggaggc gggagggagg 2050  
gaatgggggt gggctgtgcg cagcatcagc gcctggcag gtcgcagag 2100  
ctgcggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala
1					5				10					15

His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser
						20			25					30

Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp
					35				40					45

Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr
					50				55					60

Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu
					65					70				75

Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln
					80				85					90

Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu
					95				100					105

Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala
									110		115			120

Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln
					125				130					135

Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro  
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatgtt 50  
cctcttattt ctcctcacgt gtgagctggc tgcagaagtt gctgcagaag 100  
ttgagaaatc ctcagatggt cctggtgctg cccaggaacc cacgtggctc 150  
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200  
cataggcttc ttccaggatt tagaaatacc agcagtgcac atactccata 250  
gcatggtgca aaaattccca ggctgtcat ttgggatcag cactgattct 300  
gaggttctga cacactacaa catcaactggg aacaccatct gcctcttcg 350  
cctggtagac aatgaacaac tgaattttaga ggacgaagac attgaaagca 400  
ttgatgccac caaattgagc cgtttcattt agatcaacag cctccacatg 450  
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500  
tcagattcat ctcctcctga taatgaacaa ggctccccca gagtatgaag 550  
agaacatgca cagataccag aaggcagcca agctcttcca gggaaagatt 600  
ctctttattt tggggacag tggatgaaa gaaaatgggaa aggtgatatc 650  
atttttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700  
ctcttagatga cgagtggat acactgccc cagcagaagt ttccgttagag 750  
catgtgcaaa acttttgtga tggattccta agtggaaaat tggaaaga 800  
aaatcgtgaa tcagaaggaa agactccaaa ggtggaaactc tgacttctcc 850  
ttggaaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900  
aactcaaatc tcagagacac taaacaacag gatcaactgg cctgccaacc 950  
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000  
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgaaa 1050  
tctcttcttc cttctttaa attcatatc ctcactccct atccaaatttc 1100  
cttcttatcg tgcattcata ctctgtaaac ccatactgtaa cacacctaga 1150  
tcaaggcttt aagagactca ctgtgtatgcc tctatgaaag agaggcattc 1200

ctagagaaaat attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250  
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300  
gttgaaactc tactttctt cataaggcaca tgtccgtctc tgactcagga 1350  
tcaaaaacca aaggatggtt taaacacacct ttgtgaaatt gtcttttgc 1400  
cagaagttaa aggctgtctc caagtcctg aactcagcag aaatagacca 1450  
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaatcaa 1500  
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser  
200 205 210  
Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr  
215 220 225  
Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val  
230 235 240  
Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly  
245 250 255  
Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys  
260 265 270  
Val Glu Leu

<210> 359  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 359  
ccagcagtgc ccatactcca tagc 24

<210> 360  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 360  
tgacgagtggtt gatacactgc 20

<210> 361  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 361  
gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattcttag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
ggagagccgc ggctgggacc ggagtgggaa gcgcggcgta gaggtgccac 50  
ccggcgccgg tggcgagag atcagaagcc tcttccccaa gccgagccaa 100  
cctcagcgaa gacccgggct cagggacgcg gcggcgccgg cgccgactgc 150  
agtggcttga cgatggcagc gtccgcggaa gccggggcggt tgattgcagc 200  
cccagacagc cggcgctggc tgtggcggt gctggcgccg ggcgttggc 250  
tcttgacagc tggagtatca gccttggaaat tatatacgcc aaaagaaaatc 300  
ttcgtggcaa atggcacaca agggaaagctg acctgcaagt tcaagtctac 350  
tagtacgact ggcgggttga cctcagtcctc ctggagcttc cagccagagg 400  
ggccgcacac tactgtgtcg ttttccact actcccaagg gcaagtgtac 450  
cttggaaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
tgacaagaaa gatgcataa tcaacataga aaatatgcag ttatatacaca 550  
atggcaccta tatctgttat gtcaaaaacc ctccgtacat cggtgtccag 600  
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgccgtgttt 650  
tccagttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700  
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
aaacgggatt acactggctg cagtagatca gagagttgt caccagttaa 800  
gcaggctctt cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850  
tgccttctgg atctcaccag gcccagtca tatatgcaca gtttagaccac 900  
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950  
tgcggatatc cgaaagaatt aagagaatac cttagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtac ccattaccac 1050  
atgttagcctt ggagaccocag gcaaggacaa gtacacgtgt actcacagag 1100  
ggagagaaaag atgtgtacaa aggatatgtta taaatattct atttagtcat 1150  
cctgatatacga ggagccagtgttgcatgtatgaaaagatggatgattctac 1200  
atatgtaccc attgtcttgc tgttttgtatcttctttc aggtcattta 1250  
caattggagatttcagaaa catttcatttc accatcattt agaaatggtt 1300  
tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350  
ccttttaatc taaggccta agactgatta gtcttagcat ttactgttagt 1400  
tggaggatgg agatgctatg atggaagcat acccagggtg gccttagca 1450  
cagtatcagt accatttatt tgtctgccgc ttttaaaaaa tacccattgg 1500  
ctatgccact tgaaaacaat ttgagaagtt ttttgaagt ttttctcact 1550  
aaaatatggg gcaattgtta gccttacatgttgttagac ttactttaag 1600  
tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700  
tcaatactga ttaagttagaa aatccaagct ttgcttgaga acttttgtaa 1750  
cgtggagagt aaaaagtatc ggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met	Ala	Ala	Ser	Ala	Gly	Ala	Gly	Ala	Val	Ile	Ala	Ala	Pro	Asp
1				5					10				15	

Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Ala	Leu	Gly	Leu
				20				25				30		

Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
				35				40				45		

Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
				50					55			60		

Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
					65				70			75		

Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
					80				85			90		

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp
				95					100			105		

Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile
			110						115					120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys
			125						130					135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile
			140						145					150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val
			155						160					165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr
			170						175					180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn
			185						190					195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser
			200						205					210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly
			215						220					225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile
			230						235					240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile
			245						250					255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn	
			260						265					

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

```

gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
cgggctgccg ccccccgggg ctggcctca agctgcggac gacgcggggt 100
ccatcagcgc gccgggctgc cgccctctcg ccacggctgg gtcgggggcc 150
tcgggctggg gctgggctg gcgcctgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccgccca gtcccccgcg gcccccgacc ctgaggcgtc 250
gcctctggcc gagccgcac aggagcagtc cctcgccccg tggctccgc 300
agaccccgcc gcccgcctgc tccaggtgct tcgcccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
agtggtttggaa gtttctgttag atggaaaaga agtctggtca gaaggtttag 450
gttatgctga tggagaaac cgtgtaccat gtaaaccaga gacagttatg 500

```

cgaattgcta gcatcagcaa aagtctcacc atgggtgctc ttgccaatt 550  
gtggaagca gggaaactgg atcttgatata tccagttacaa cattatgttc 600  
ccgaattccc agaaaaagaa tatgaaggtg aaaaggtttgc tgtcacaaca 650  
agattactga tttcccatat aagtggatt cgtcattatg aaaaggacat 700  
aaaaaaaggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750  
agaatgtgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850  
ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900  
tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt attaaaaat 950  
gatccttgc tcttcaaacc tgtagtcag ttttgtatt caactttgg 1000  
ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaatatt 1050  
tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100  
caggaagaaa acgagccagt gatttacaat agagcaaggt aaatgaatac 1150  
cttctgctgt gtctagctat atcgcatctt aacactatatt tattaattaa 1200  
aagtcaaatt ttcttgaaaat ccattccaaa atcaacctgc cacattttgg 1250  
gagctttct acatgtctgt tttctcatct gttaagtgaa ggaagtaaaa 1300  
catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro  
1 5 10 15

Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg  
20 25 30

Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly  
35 40 45

Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu  
50 55 60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu  
65 70 75

Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro  
80 85 90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala
					95				100					105
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp
					110				115					120
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly
					125				130					135
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn
					140				145					150
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile
					155				160					165
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala
					170				175					180
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu
					185				190					195
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr
					200				205					210
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys
					215				220					225
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys
					230				235					240
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys
					245				250					255
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu
					260				265					270
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn
					275				280					285
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn
					290				295					300
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe
					305				310					315
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu
					320				325					330
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp
					335				340					345
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val
					350				355					360
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg		
					365				370					

<210> 367

<211> 30  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-30  
<223> Synthetic construct.

<400> 367  
tggaaaagaa gtctggtcag aaggtagg 30

<210> 368  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 368  
catttggctt cattctccctg ctctg 25

<210> 369  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 369  
aaaacacctcag aacaactcat tttgcacc 28

<210> 370  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-41  
<223> Synthetic construct.

<400> 370  
gtctcaccat gtttgctttt gccaaattgt gggaaaggcagg g 41

<210> 371  
<211> 1150  
<212> DNA  
<213> Homo sapiens

<400> 371  
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctgggt gggagaagc cgagatggcg gcagccagcg 100  
ctggggcaac ccggctgctc ctgtcttgc tcatggcggt agcagcgccc 150  
agtgcagccc ggggcagcgg ctgccggcc gggactggtg cgcgaggggc 200  
tggggcggaa ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250  
tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300  
tcactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350  
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450  
gaagctggtg gctatgtctc ctcccttgc cctgcgtgt ccctggtgaa 500  
gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550  
tgggtggcgt gtcgggtggtg acgcaccccg ggggctgccc gggccatgag 600  
gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650  
gccaccaca gccccaggcc ctgagacggc ggccttcatt gagcgcctgg 700  
agatggaaca ggcccagaag gccaagaacc cccaggagca gaagtccttc 750  
ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800  
gtcaggagcg ccagacacccg ggggccaggg tgggggtggg ggtgggggtg 850  
gtggtggggg tagtggcctt tgctgtgtc caccctccct gtaagtctat 900  
ttaaaaacat cgacgataca ttgaaatgtg tgaacgttt gaaaagctac 950  
agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000  
tacaagcttg attgaaattc actgctcaact tgatacgtta ttcagaaacc 1050  
caaggaatgg ctgtccccat cctcatgtgg ctgtgtggag ctcagctgtg 1100  
ttgtgtggca gtttattaaa ctgtccccca gatcgacacg caaaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1														15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
														30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
														45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe
						50			55					60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu
						65			70					75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu
						80			85					90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn
						95			100					105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp
						110			115					120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys
						125			130					135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val
						140			145					150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro
						155			160					165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu
						170			175					180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly
						185			190					195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala
						200			205					210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys
						215			220					225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser
						230			235					240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly						
						245			250					255
Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
						260			265					

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaaacccga gccggagccg gagccacagc ggggagggtg 50

gcctggcgcc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150

tgttaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctaaaccccc tggaaaggccc tgcagcaatc cctccttcct tcggtttcaa 250  
ctggacttct atcaggctcta ctccctggcc ctggcagctg attggcttca 300  
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350  
aaattgccat cctctatgtc tgtggcttg cctctacagt cctctttggc 400  
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450  
cctcttctcc ctgacttact cactatgctg cttaacccaa ctctctcaag 500  
actactttgt gctgcttagtg gggcgagcac ttgggtggct gtccacagcc 550  
ctgctcttct cagccttcga ggcctggtat atccatgagc acgtggaacg 600  
gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650  
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700  
gccagctgga tagggctggg gcctgttagcg ccctttgtgg ctgccatccc 750  
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800  
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850  
ctcctgtcgg accgcccgcgt gctgctgctg ggcaccatac aagctctatt 900  
tgagagtgtc atcttcatct ttgtcttcct ctggacacacct gtgctggacc 950  
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000  
ctgcttggct cttccctgtta ccgtatcgcc acctccaaga ggtaccacct 1050  
tcagccccatg cacctgctgt ccctgctgt gctcatcgtc gtcttctctc 1100  
tcttcatgtt gactttctct accagcccag gccaggagag tccgggtggag 1150  
tccttcatag cctttctact tattgagttt gcttgtggat tatactttcc 1200  
cagcatgagc ttcctacgga gaaaggtgat ccctgagaca gagcaggctg 1250  
gtgtactcaa ctggttccgg gtacctctgc actcaactggc ttgccttaggg 1300  
ctccttgc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350  
cagcatttgc tctgctgtca tggtgatggc tctgctggca gtgggtggac 1400  
tcttcaccgt ggttaaggcat gatgctgagc tgcgggtacc ttcacctact 1450  
gaggagccct atgcccctga gctgtaaccc cactccagga caagatacg 1500  
gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550  
gactgacttt gtgactgtcc tgtggttct cctgccattg ctttgtttt 1600  
gggaggacat gatgggggtg atggactgga aagaagggtgc caaaagttcc 1650

ctctgtgtta ctccccattha gaaaataaac acttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser  
1 5 10 15

Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly  
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe  
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Asp Trp Leu Gln Ala  
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly  
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu  
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys  
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu  
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala  
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala  
140 145 150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu  
155 160 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val  
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp  
185 190 195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu  
200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn  
215 220 225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu  
230 235 240

Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile
				245					250					255
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp
				260					265					270
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe
				275					280					285
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg
				290					295					300
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu
				305					310					315
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr
				320					325					330
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile
				335					340					345
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser
				350					355					360
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala
				365					370					375
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys
				380					385					390
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr
				395					400					405
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu
				410					415					420
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu
				425					430					435
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu
				440					445					450

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

gcgacgcgcg gcggggcgcc gagagaaac gcggcgccgg gccgggcccc 50

gccctggaga tggtccccgg cgccgcggc tggtgtgtc tcgtgctctg 100

gctccccgcg tgcgtcgccg cccacggctt ccgtatccat gattatttgt 150

actttcaagt gctgagtcct gggacattc gatacatctt cacagccaca 200

cctgccaagg actttggtgg tatcttcac acaaggatg agcagattca 250

ccttgcctcc gctgaacctc cagaggcctg cggggactc agcaacgggtt 300  
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctcccttc 350  
ctctccaaga ctcggtggt ccaggagcac ggcgggcggg cggtgatcat 400  
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450  
acagtaccca ggcacagct gacatccccg ccctttcct gctggccga 500  
gacggctaca tgcgtccggc ctctctggaa cagcatggc tgccatggc 550  
catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600  
tgcaaccgcc ctggaccccttc tggtagaaga gtttgtccca cattccagcc 650  
ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750  
tttggcggt gctaggctga aagggaaagcc acaccactgg cttcccttc 800  
cccaggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850  
ccccaggcgt tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900  
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctccccc 950  
tacccagggt ctctgcacag tgacccctcac agcagttgtt ggagtggttt 1000  
aaagagctgg tgtttgggaa ctcaataaac cctcactgac ttttagcaa 1050  
taaagcttct catcagggtt gaaaaaaaaaaaaaaaaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1														15

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
														30

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
														45

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Ile	Phe	His	Thr	Arg	Tyr	
														60

Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
														75

Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
														90

Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln
				95					100					105
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp
				110					115					120
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg
				125					130					135
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr
				140					145					150
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile
				155					160					165
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu
				170					175					180
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp							
				185										

<210> 377

<211> 496

<212> DNA

<213> Artificial

<220>

<221> unsure

<222> 396

<223> unknown base

<400> 377

tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50

ggctgggtggt gatggctgggt gtgattccaa tccagggcgg gatcctgaac 100

ctgaacaaga tggtaagca agtgactggg aaaatgccc tcccttccta 150

ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200

atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250

aagacccagg ggtgcggcat ctacaaggac aacaacaaaaa gcagcataca 300

ttgtatggat ttatctcaac gctattgttt aatggctgtg ttatgtga 350

tctatctgga aaatgaggac tccgaataaa aagctattac tawtnaaaa 400

aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 450

aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val  
1 5 10 15

Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys  
20 25 30

Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly  
35 40 45

Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr  
50 55 60

Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys  
65 70 75

Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile  
80 85 90

His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe  
95 100 105

Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu  
110 115

<210> 379  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 379  
ctgcctccac tgctctgtgc tggg 24

<210> 380  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 380  
cagagcagtg gatgttcccc tggg 24

<210> 381  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45

<223> Synthetic construct.

<400> 381  
ctgaacaaga tggtaagca agtgactggg aaaatgccc tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382  
ctcgcttctt cttctggat gggggccag ggggcccagg agagtataaa 50  
ggcgatgtgg agggtgcccc gcacaaccag acgcccagtc acaggggaga 100  
gccctggat gcaccggcca gagccatgc tgctgctgct cacgcttgcc 150  
ctcctgggg gccccacctg ggcaggaaag atgtatggcc ctggaggagg 200  
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250  
gggtgtctgt aggtcttctc ctggtaaaaa gtgtccaggt gaaacttgg 300  
gactcctggg acgtgaaact gggagccta ggtggaaata cccaggaagt 350  
cacccctgcag ccaggcgaat acatcacaaa agtcttgc tccttccaag 400  
cttcctccg gggtatggtc atgtacacca gcaaggaccg ctatttctat 450  
tttgggaagc ttgatggcca gatctcctt gcctacccca gccaaagagg 500  
gcaggtgctg gtgggcataat atggccagta tcaactcctt ggcataaga 550  
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600  
ccagttataatc tcacatactc agcaaactca cccgtgggtc gctagggtgg 650  
ggtatggggc catccgagct gaggccatct gtgtgggtgg ggctgatgg 700  
actggagtaa ctgagtcggg acgctgaaatc tgaatccacc aataaataaa 750  
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383  
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu  
1 5 10 15  
Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly  
20 25 30  
Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr  
35 40 45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln
														50
														55
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly
														65
														70
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr
														80
														85
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met
														95
														100
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly
														110
														115
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val
														125
														130
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly
														140
														145
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro
														155
														160
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg		
														170
														175

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

gctgagcgtg tgcgcggtag ggggctctcc tgccttcgtt gctccaacgc 50

agctctgtgg ctgaactggg tgctcatcac gggaaactgct gggctatgg 100

atacagatgt ggcagctcag gtagccccaa attgcctggg agaatacata 150

atgtttttcg ataagaagaa attgttaggat ccagttttt ttttaaccgc 200

ccccctccccca ccccccggaaa aaactgtaaa gatgcgggggg cgtaatatcc 250

atgaagatcc tattacctag gaagattttt atgttttgct gcgaatgcgg 300

tgttgttggatt tattttgttct tggagtgttc tgcgtggctg gcaaagaata 350

atgttccaaa atcgggtccat ctcccaagggt gtccaaatttt tcttcctggg 400

tgtcaggcgag ccctgactca ctacagtgcgac gctgacaggg gctgtcatgc 450

aactggccccc taagccaaag caaaagaccc aaggacgacc tttgaacaat 500

acaaaggatg ggtttcaatg taatttaggct actgagcggg tcagctgttag 550

cactggttat agcccccaact gtcttactga caatgcttcc ttctgccgaa 600

cgaggatgcc ctaagggctg taggtgtgaa ggcaaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tataatctgct ggttgcttag 700  
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750  
aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800  
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850  
ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900  
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcatctct 950  
gggatctgaa cagtttcggg gctgcggaa gctgctgagt ttacatttac 1000  
ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050  
aacctggaac ttttggacct gggatataac cgatccgaa gtttagccag 1100  
aatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150  
atcaattttc caagctcaac ctggcccttt ttccaagggtt ggtcagcctt 1200  
cagaaccttt acttgcagtg gaataaaatc agtgtcatag gacagaccat 1250  
gtcctggacc tggagctcct tacaaggct tgatttatca ggcaatgaga 1300  
tcgaagcttt cagtgacccc agtgtttcc agtgtgtccc gaatctgcag 1350  
cgcctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400  
ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450  
aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagtttaaa 1500  
ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550  
agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600  
ctacagagag gtttgatctg gccaggcgtc tcccaaagcc gacgtttaag 1650  
cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgcccccgac 1700  
ggtgggagcc acagagccccg gcccagagac cgatgctgac gcccagcaca 1750  
tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800  
ctcgtcatcc tgctggttat ctacgtgtca tggaagcggt accctgcgag 1850  
catgaagcag ctgcagcagc gctccctcat gcgaaggcac agaaaaaaga 1900  
aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta 1950  
gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatggac 2000  
gggaccctgc acctataaca aatcggcgtc cagggaggtt gaggtatgaa 2050  
ccattgtat aaaaagagct cttaaaagct gggaaataag tggtgcttta 2100

ttgaactctg gtgactatca aggaaacgac atgcggccccc tccccttccc 2150  
tctccctctc actttggtgg caagatcctt ccttgcgttccgt ttttagtgcatt 2200  
tcataatact ggtcattttc ctctcataaca taatcaaccc attgaaattt 2250  
aaataccaca atcaatgtga agcttgaact ccgggttaat ataataccta 2300  
ttgtataaga ccctttactg attccattaa tgtcgcat tt gtttaagat 2350  
aaaacttctt tcataaggtaa aaaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala  
1 5 10 15

Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala  
20 25 30

Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val  
35 40 45

Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser  
50 55 60

Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys  
65 70 75

Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu  
80 85 90

Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe  
95 100 105

Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg  
110 115 120

Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu  
125 130 135

Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser  
140 145 150

Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg  
155 160 165

Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys  
170 175 180

Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser  
185 190 195

Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

	200	205	210
His Leu Glu His Asn Gln Phe Ser Lys			
215	220	225	
Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr			
230	235	240	
Ile Ser Val Ile Gly Gln Thr Met Ser Trp			
245	250	255	
Gln Arg Leu Asp Leu Ser Gly Asn Glu			
260	265	270	
Pro Ser Val Phe Gln Cys Val Pro Asn Leu			
275	280	285	
Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln			
290	295	300	
Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala			
305	310	315	
Cys Ser Arg Asn Ile Cys Ser Leu Val Asn			
320	325	330	
Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys			
335	340	345	
Leu Gln Gly Val Asn Val Ile Asp Ala Val			
350	355	360	
Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp			
365	370	375	
Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro			
380	385	390	
Ser Lys Pro Pro Leu Pro Pro Thr Val Gly			
395	400	405	
Pro Glu Thr Asp Ala Asp Ala Glu His Ile			
410	415	420	
Ile Ala Gly Ser Val Ala Leu Phe Leu Ser			
425	430	435	
Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr			
440	445	450	
Gln Leu Gln Gln Arg Ser Leu Met Arg Arg			
455	460	465	
Arg Gln Ser Leu Lys Gln Met Thr Pro Ser			
470	475	480	
Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr			
485	490	495	

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu  
500 505 510

Cys Glu Val

<210> 386  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 386  
ctgggatctg aacagttcg gggc 24

<210> 387  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 387  
ggtccccagg acatggtctg tccc 24

<210> 388  
<211> 48  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-48  
<223> Synthetic construct.

<400> 388  
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389  
<211> 1449  
<212> DNA  
<213> Homo sapiens

<400> 389  
agttctgaga aagaaggaaa taaacacagg caccaaacc caatcctaag 50  
ttgactgtcc tttaaatatg tcaagatcca gactttcag tgtcacctca 100  
gcgatctcaa cgatagggat cttgtgttg ccgctattcc agttggtgct 150  
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggat atctggatcc tcctgctgct ggtttggtg 250  
gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300  
gagaccccga attgattctc acaggcgcac catggcagtt tttgctgtt 350  
gagacttgga ctctatttat gggacagaag cagctgtgag tccaaactgtt 400  
ggaattcacc ttcaaactca aaccctgac ctatatcctg ttccctgctcc 450  
atgtttggc ccttagct ccccacctcc atatgaagaa attgtaaaaa 500  
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550  
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600  
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaaagaat 650  
ggatgttgga aaaaattttg gtcatggaga tgtttaataa gtaaagtagc 700  
aggctttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750  
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800  
gtagttcca tcacatttag gactccactg cagtatacag cacaccattt 850  
tctgcttaa actcttcct agcatgggt ccataaaaat tattataatt 900  
taacaatagc ccaagccgag aatccaaacat gtccagaacc agaaccagaa 950  
agatagtatt tgaatgaagg tgagggaga gagtaggaaa aagaaaagtt 1000  
tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050  
gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100  
tgtagataga aggtgaagga gattgctgaa gatatacagc acatataatg 1150  
ccaacacggg gagaaaagaa aatttccccct tttacagtaa tgaatgtggc 1200  
ctccatagtc catagtgtt ctctggagcc tcagggcttgc gcatttattt 1250  
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
gcagaagtag caatgagaca tcttcaagtgc gcattttggc agtggccatc 1350  
agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400  
ctgacaaatt tggtaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1					5				10					15

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp
						20				25				30
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln
							35			40				45
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu
						50			55					60
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys
						65			70					75
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala
						80			85					90
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala
						95			100					105
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro
						110			115					120
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser
						125			130					135
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr				
						140			145					

<210> 391

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 391

cttttcagtg tcacacctcagc gatctc 26

<210> 392

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 393  
ccagttggtg ctctcgacc taccatgcga agaagatgaa atgtgtg 47

<210> 394  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 394  
gagcggagta aaatctccac aagctggaa caaacctcgt cccaactccc 50  
acccacccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100  
gacgcagctg acgccccgtt attagctctc gctgcgtcgc cccggctcag 150  
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200  
tctcttctac tttgggagag agagaaaagtc agatgccct tttaaactcc 250  
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggataacaac 300  
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350  
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400  
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450  
tatgtcccag aaattgagtt tactgttgct tgtatttggg ctcatttggg 500  
gattgatgtt actgcactat actttcaac aaccaagaca tcaaaggcagt 550  
gtcaagttac gtgagcaaact actagactta agcaaaagat atgttaaagc 600  
tctagcagag gaaaataaga acacagtgg tgctgagaac ggtgcttcta 650  
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700  
attttgcac gattggtgaa gctggagaac aaagttgact atatttgtt 750  
gaatggctca gcagccaaaca ccaccaatgg tactagtggg aatttggc 800  
cagtaaccac aaataaaaga acgaatgtct cgggcagttt cagatagcag 850  
ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900  
agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950  
aagctctaca catttcaag gagttatgctg gattcatggc actctaattc 1000  
tgtacataaa aattttaaag ttatttgttt gctttcaggc aagtctgttc 1050  
aatgctgtac tatgtccctta aagagaattt ggtaacttgg ttgatgtggt 1100

aagcagatag gtgagtttg tataaatctt ttgtgttga gatcaagctg 1150  
aaatgaaaac actgaaaaac atggattcat ttctataaca catttattta 1200  
agtatataac acgtttttg gacaagtcaa gaatgtttaa tcattctgtc 1250  
atttgttctc aatagatgta actgttagac tacggctatt tgaaaaaatg 1300  
tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350  
tataatgttgc 1400  
tttgcaactat ccttcagaat aactgaaggt taattattgt atattttaa 1450  
aaattacact tataagagta taatcttgc 1500  
attacctatc gtaaacattt gggcaatttataa acatcagcat taaaatagtt 1550  
gtaaactcta atcttataact tattgaagaa taaaagatat ttttatgtg 1600  
agagtaacaa taaagtatttgc 1650  
aaaagtttaa tccttgagt gtctatgcta tcagggaaagc acattatttc 1700  
catatttggg ttaattttgc ttttattata ttgggtctagg aggaagggac 1750  
tttggagaat ggaactcttg aggacttttag ccaggtgtat ataataaagg 1800  
tactttgttgc 1850  
taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcatttagat 1900  
attcattttta tataatggcc acttaaaata agaacatttta aaatataaac 1950  
tatgaagatt gactatctt tcagggaaaaa agctgtatag acacaggga 2000  
accctaatct tgggttaatttgc 2050  
atttcccttg tagcaaatttgc 2100  
tatttattct ctatagtaac tgcttaagtgc 2150  
actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200  
catgtacaa taattacaat attttattaa aataaatatg tgaaatattg 2250  
tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300  
acctttatgttgc 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1														15

Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu
				20					25				30	
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35					40				45	
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50					55				60	
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65					70				75	
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80					85				90	
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95					100				105	
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110					115				120	
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
				125					130				135	
Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 396  
 cgcggccggg ccgccgggt gagcgtgccg aggcggctgt ggccgcaggct 50  
 tccagcccc accatgccgt ggcccctgct gctgctgctg gccgtgagtg 100  
 gggcccagac aaccggcca tgctccccg ggtgccaatg cgaggtggag 150  
 acttcggcc tttcgacag cttcagcctg actcgggtgg attgttagcgg 200  
 cctggccccc cacatcatgc cggtgccccat ccctctggac acagcccact 250  
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300  
 gggccgggct acacgacggt ggctggcctg gatctcagcc acaacctgct 350  
 caccagcatc tcacccactg ccttctcccg cttcgctac ctggagtcgc 400  
 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450  
 agctcacccc tgagcgtacgt gaaccttagc cacaaccaggc tccgggaggt 500  
 ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550  
 acctctccca caacctcatt caccgcctcg tgccccaccc cacgagggcc 600  
 ggcctgcctg cgccccaccat tcagagcctg aacctggcct ggaaccggct 650

ccatgccgtg cccaacacctc gagacttgcc cctgcgtac ctgagcctgg 700  
atggaaaccc tctagctgtc attggtccgg gtgccttcgc gggctggga 750  
ggccttacac acctgtctct ggccagcctg cagaggctcc ctgagctggc 800  
gcccagtggc ttccgtgagc taccgggcct gcaggtcctg gacctgtcg 850  
gcaaccccaa gcttaactgg gcaggagctg aggtgtttc aggctgagc 900  
tccctgcagg agctggaccc ttccggcacc aacctggtgc ccctgcctga 950  
ggcgctgctc ctccacacctc cgccactgca gagcgtcagc gtggggcagg 1000  
atgtgcggtg ccggcgccctg gtgcgggagg gcacccatccc ccggaggcct 1050  
ggctccagcc ccaaggtgcc cctgcactgc gtagacaccc gggaaatctgc 1100  
tgccaggggc cccaccatct tgtgacaaat ggtgtggccc agggccacat 1150  
aacagactgc tgtcctggc tgcctcaggt cccgagtaac ttatgttcaa 1200  
tgtgccaaca ccagtgggga gccccgaggc ctatgtggca gcgtcaccac 1250  
aggagttgtg ggccttaggag aggctttgga cctgggagcc acacccatgg 1300  
gcaaagtctc acccccttgc ctacgttgct tccccaaacc atgagcagag 1350  
ggacttcgat gccaaaccagg actcgggtcc cctcctgctt cccttcccc 1400  
cttatcccccc aagtgccttc cctcatgcct gggccggcct gacccgcaat 1450  
gggcagaggg tgggtgggac cccctgctgc agggcagagt tcaggtccac 1500  
tgggctgagt gtccccctgg gccatggcc cagtcactca gggcgagtt 1550  
tctttctaa catagccctt tctttgccat gaggccatga ggcccgcttc 1600  
atccctttct atttccctag aacctaattg gtagaaggaa ttgcaaagaa 1650  
tcaagtccac ccttctcatg tgacagatgg ggaaactgag gccttgagaa 1700  
ggaaaaaggc taatctaagt tcctgcgggc agtggcatga ctggagcaca 1750  
gcctcctgcc tcccagcccg gacccaatgc actttcttgt ctccctcta 1800  
aagccccacc ctccccggct gggctccct tgctgcctt gcctgttccc 1850  
cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900  
gactctgggc ctctgaccag ctgtgcggca tgggctaagt cactctgccc 1950  
ttcggagcct ctggaagctt agggcacatt ggttccagcc tagccagtt 2000  
ctcacccctgg gttggggtcc cccagcatcc agactggaaa cctaccatt 2050  
ttcccccgtag catcctctag atgctgcccc aaggagttgc tgcagttctg 2100

gagcctcatc tggctggat ctccaagggg cctcctggat tcagtcccc 2150  
ctggccctga gcacgacagc ccttcttacc ctcccaggaa tgccgtgaaa 2200  
ggagacaagg tctgcccac ccatgtctat gctctacccc cagggcagca 2250  
tctcagcttc cgaaccctgg gctgtttcct tagtcttcat tttataaaag 2300  
tttgtgcctt tttaacggag tgtcacttcc aaccggcctc ccctacccct 2350  
gctggccggg gatggagaca tgtcatttgt aaaagcagaa aaaggttgca 2400  
tttgttcaact tttgtatat tgcctggc ctgtgttggg gtgttgggg 2450  
aagctggca tcagtggcca catggcatac aggggctggc cccacagaga 2500  
ccccacaggg cagttagctc tgtcttcccc cacctgccta gcccatcatc 2550  
tatctaaccg gtccttgatt taataaacac tataaaaggt ttaaaaaaaaa 2600  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met Pro Trp Pro Leu Leu Leu Leu Ala Val Ser Gly Ala Gln  
1 5 10 15

Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr  
20 25 30

Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser  
35 40 45

Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr  
50 55 60

Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu  
65 70 75

Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp  
80 85 90

Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser  
95 100 105

Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu  
110 115 120

Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp  
125 130 135

Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala  
140 145 150

Phe	Thr	Thr	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser
														155
														160
														165
His	Asn	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly
														170
														175
														180
Leu	Pro	Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg
														185
														190
														195
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu
														200
														205
														210
Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe
														215
														220
														225
Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln
														230
														235
														240
Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly
														245
														250
														255
Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala
														260
														265
														270
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp
														275
														280
														285
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu
														290
														295
														300
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg
														305
														310
														315
Cys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly
														320
														325
														330
Ser	Ser	Pro	Lys	Val	Pro	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser
														335
														340
														345
Ala	Ala	Arg	Gly	Pro	Thr	Ile	Leu							
														350

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaagggcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caaccccaag cttaactggg caggagctga ggtgtttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgcag ccacagcttc tgtgagattc gatttctccc cagttcccc 50

gtqggctctga ggggaccaga agggtagct acgttggctt tctggaaagg 100

gaggctatat gcgtcaattc cccaaaacaa gtttgacat ttccccctgaa 150

atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

ctgctggca ctaacggcg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttggaaagct gtgtgatcgc cacaaacctt cagggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tcttgcaag acacaaagcc tgcgaatcga 600

tgctgcctcc tgcgccattt gctaagactc tatctggaca gggattttaa 650

aaactaccag acccctgacc attatactct ccggaaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750

atgacatgcc attgtggga ggaagcaatg aagaaataca gccagattct 800  
gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggcttgg 850  
gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900  
agtatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950  
acctgcagag gaggcatgac cccaaaccac catctcttta ctgtactagt 1000  
cttgtgctgg tcacagtgtt tcttattttt gcattacttg cttccttgca 1050  
tgattgtctt tatgcattccc caatcttaat tgagaccata cttgtataag 1100  
atttttgtaa tatctttctg ctattggata tatttatttag ttaatatatt 1150  
tatttatttt ttgctattta atgtatTTT tttttactt ggacatgaaa 1200  
ctttaaaaaa attcacagat tatattata acctgactag agcaggtgat 1250  
gtattttat acagtaaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300  
ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350  
gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400  
tgtgaaataa gtttgatgt ggaattgcac atctacctt caattactga 1450  
ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550  
ccaaaaaaaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1				5					10				15	

Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
					20				25				30	

Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
					35			40					45	

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
					50			55					60	

Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
					65				70				75	

Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
					80				85				90	

<210> 403  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 403  
ctcctgtggt ctccagattt caggccta 28

<210> 404  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 404  
 agtcctcctt aagattctga tgtcaa 26

<210> 405  
 <211> 998  
 <212> DNA  
 <213> Homo sapiens

<400> 405  
 ccgttatcgt cttgcgtac tgctgaatgt ccgtcccgga ggaggaggag 50  
 aggctttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100  
 gtccggctgc gcggctaccg tggccgagct agcaaccctt cccctggatc 150  
 tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
 ggagacggtg caagagaatc tgccccctat agggaaatgg tgcgcacagc 250  
 cctagggatc attgaagagg aaggcttct aaagcttgg caaggagtga 300  
 caccgcacat ttacagacac gtagtgtatt ctggaggctcg aatggtcaca 350  
 tatgaacatc tccgagaggt tggtttggc aaaagtgaag atgagcatta 400  
 tcccccttgg aaatcagtca ttggagggat gatggctgg tttattggcc 450  
 agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500  
 ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
 tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttggcag 600  
 gctgggtacc caatatacaa agagcagcac tggtaatat gggagattta 650  
 accacttatg atacagtcaa acactacttg gtattgaata caccacttga 700  
 ggacaatatc atgactcactg gtttatcaag tttatgttct ggactggtag 750  
 cttctattct ggaaacacca gccgatgtca tcaaaagcag aataatgaat 800  
 caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
 ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900  
 gcttttacc atcttggctg agaatgaccc cttggtaat ggtttctgg 950  
 cttaacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 406  
 Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln  
 1 5 10 15

Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala
				20				25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
				35				40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
				50				55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
				65				70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80				85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg
				95				100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser
				110				115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met
				125				130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu
				140				145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly
				155				160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile
				170				175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro
				185				190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
				200				205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
				215				220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
				230				235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
				245				250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr
				260				265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly
				275				280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met
				290				295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe  
320

<210> 407  
<211> 31  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-31  
<223> Synthetic construct.

<400> 407  
cgccggatccc gttatcgctc tgcgctactg c 31

<210> 408  
<211> 34  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-34  
<223> Synthetic construct.

<400> 408  
gcggaattct taaaatggac tgactccact catc 34

<210> 409  
<211> 1487  
<212> DNA  
<213> Homo sapiens

<400> 409  
cgacgcgtg ggccgggac gccggcaggg ttgtggcgca gcagtctcct 50  
tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctggata 100  
cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggottcc 150  
tagataattt tcgttggcca gaatgtaat gtattgactg gagtgagaga 200  
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250  
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300  
accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350  
ataaatgctg tatccaatgc tcaggtgaga ggtgataagct atgaaagcgg 400  
ctgttttagga agaacaggtg ctgcgatggc gctttcatt ggtttcatgt 450  
tgcgtttgg gtcacttatt gctccatgt ggattctttt tggtgcatat 500  
gttacccaaa atactgatgt ttatccggga ctagctgtgt ttttcaaaa 550

tgcaacctata ttttttagca ctctgatcta caaatttggaa agaaccgaag 600  
agctatggac ctgagatcac ttcttaagtc acatttcct tttgttatat 650  
tctgtttgtta gatagggttt ttatctctca gtacacattt ccaaatggag 700  
tagattgtac attaaatgtt ttgtttttt acattttat gttctgagtt 750  
ttgaaatagt tttatgaaat ttcttttattt ttcattgcat agactgttaa 800  
tatgtatata atacaagact atatgaattt gataatgagt atcagtttt 850  
tattcctgag atttagaact tgatctactc cctgagccag ggttacatca 900  
tcttgcatt ttagaagtaa ccactcttgt ctctctggct gggcacggtg 950  
gctcatgcct gtaatcccag cactttggaa ggccgaggcg ggccgattgc 1000  
ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050  
tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100  
cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150  
aggttgcagt gagctgagtt tgccgcactg cactctagcc tgggggagaa 1200  
agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250  
gaagatgtac aaaaaaatat agttcatat atctggaatg agcactgagc 1300  
cataaaaggt tttcagcaag ttgttaactt ttttggccta aaaatgaggt 1350  
tttttggta aagaaaaat atttgttctt atgtattgaa gaagtgtact 1400  
tttatataat gattttttaa atgccccaaag gactagtttggaa 1450  
ttaaaaagaa ttcctctaataat atgactttat gtgagaa 1487

<210> 410  
<211> 158  
<212> PRT  
<213> Homo sapiens

<400> 410  
Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys  
1 5 10 15  
Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala  
20 25 30  
Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala  
35 40 45  
Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr  
50 55 60  
Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val  
65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu  
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu  
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala  
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe  
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe  
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr  
155

<210> 411  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 411  
gtttgaggaa gctgggatac 20

<210> 412  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 412  
ccaaactcgaa gcacaccttgc 20

<210> 413  
<211> 40  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-40  
<223> Synthetic construct.

<400> 413  
atggcaggct tccttagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337  
<212> DNA  
<213> Homo sapiens

<400> 414  
gttcatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50  
gcagctggcc cactggcgcc ccgcaacact ccgtctcacc ctctggccc 100  
actgcacatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150  
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200  
gggacacctacg gcacctgctg gaccacctcg cttctccat cgaagcaggg 250  
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300  
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggcctcatac 350  
tttgcctatag tcacgacatg gatgtttatt cgaagctaca tgagcttag 400  
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450  
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500  
aactactttg cgtttaaatat ctgcagtggg gccgccaacg tcgtggccc 550  
tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600  
tggcagagg cctaaacatc gccctggta atggaaccac gggagctgtg 650  
ctggacaga aggcatgttga catgtactct ggagatgtta tgcacctagt 700  
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctct 750  
acgacgatcc agggaccaaa atgaacgatg aaagcagggaa actcttctct 800  
gacttgggaa gttcctacgc aaaacaactg ggcttccggg acagctgggt 850  
cttcatagga gccaaagacc tcagggtaa aagccccctt gaggcgttct 900  
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950  
gagatggagg gctgcacgcc cccgaagcca ttttagggtg gctgtggctc 1000  
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050  
ccggcaggg gctgaggagg aggagcaggg ggtgctgcgt ggaaggtgct 1100  
gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150  
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200  
accagctgtc tgtggagaga atgggggtct ttgcgtcaggg actgctgacg 1250  
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300  
tattttgct ggtttgaaa aaaaaaaaaa aaaaaaaaa 1337

<210> 415  
<211> 224  
<212> PRT  
<213> Homo sapiens

<400> 415  
Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala  
1 5 10 15  
Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser  
20 25 30  
Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr  
35 40 45  
Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro  
50 55 60  
Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala  
65 70 75  
Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met  
80 85 90  
Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu  
95 100 105  
Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp  
110 115 120  
Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu  
125 130 135  
Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro  
140 145 150  
Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu  
155 160 165  
Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val  
170 175 180  
Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln  
185 190 195  
Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro  
200 205 210  
Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe  
215 220

<210> 416  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence

<222> 1-21  
<223> Synthetic construct.

<400> 416  
gccatagtca cgacatggat g 21

<210> 417  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 417  
ggatggccag agctgctg 18

<210> 418  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 418  
aaagtacaag tgtggcctca tcaaggc 26

<210> 419  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 419  
tctgactcct aagtcaaggca ggag 24

<210> 420  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 420  
attctctcca cagacagctg gttc 24

<210> 421  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 421  
gtacaagtgt ggcctcatca agccctgccccc agccaactac tttgcg 46

<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1528  
<223> unknown base

<400> 422  
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50  
tgtcctgggg atccagaaac ccatgataacc ctactgaaca ccgaatcccc 100  
tggaaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150  
cacgccagga gctcgctcgc tctctctc tctctctcac tcctccctcc 200  
ctctctctct gcctgtccta gtcccttagt cctcaaattc ccagtccct 250  
gcaccccttc ctgggacact atgttgttct ccgcctcct gctggaggtg 300  
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350  
acatggtcag gaccattggc cagccttta ccctgagtg ggaaacaatg 400  
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450  
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccccc 500  
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550  
tgtatctggg tggacttccc cgaaaatatg tagctgcccc gctccacctg 600  
cactggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650  
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700  
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750  
ggcatcctaa ttgaggtggg tgagactaag aatatacgat atgaacacat 800  
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccc aacagctggg gcagtacttc 900  
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950  
gacagtttt tatagaaggc cccagatttc aatggaacag ctggaaaagc 1000  
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050  
cagaactacc gagcccttca gcctctcaat cagcgcatgg tcttgcttc 1100  
tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150  
gtgttagaat ctgggttggc tgtctctgcc ttctcctggc tgtttatttc 1200  
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtgg 1250  
cttcaccta gcacaagcca cgactgaggc ataaattcct tctcagatac 1300  
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350  
gggtgttagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400  
ccttcccctg gacatctt agagaggaat ggacctcaggc tgtcattcca 1450  
ggaagaactg cagagcccttc agcctctcca aacatgtagg agggaaatgag 1500  
gaaatcgctg tggtttaat gcagagana aactctgttt agttgcaggg 1550  
gaagtttggg atataccca aagtcctcta cccctcact tttatggccc 1600  
tttccctaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650  
gaagttgtat atttttgcgc aatatatttg gaaattaaag ttcttgactt 1700

t 1701

<210> 423  
<211> 337  
<212> PRT  
<213> Homo sapiens

<400> 423  
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala  
1 5 10 15  
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
20 25 30  
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
35 40 45  
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
50 55 60  
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
65 70 75  
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80	85	90
Pro Ser Thr Leu Tyr	Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala
95	100	105
Ala Gln Leu His Leu His Trp	Gly Gln Lys Gly Ser Pro Gly Gly	
110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu His	
125	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr Asp	Ser Leu Ser Glu Ala	
140	145	150
Ala Glu Arg Pro Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile Glu	
155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser His	
170	175	180
Leu His Glu Val Arg His Lys Asp Gln	Lys Thr Ser Val Pro Pro	
185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr Phe	
200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser Val	
215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu Gln	
230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu Pro	
245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu Asn	
260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser Tyr	
275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly	Val Gly Ile Leu Val Gly	
290	295	300
Cys Leu Cys Leu Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys Ile	
305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys	Ser Val Val Phe Thr Ser	
320	325	330
Ala Gln Ala Thr Thr Glu Ala		
335		

<210> 424  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 424  
gtaaagtgc tggccagc 18

<210> 425  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 425  
cccgatctgc ctgctgtt 18

<210> 426  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 426  
ctgcactgtt tggccattat tgtt 24

<210> 427  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 427  
cagaaaccca tgatacccta ctgaacaccc aatccccctgg aagcc 45

<210> 428  
<211> 1073  
<212> DNA  
<213> Homo sapiens

<400> 428  
aattttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50  
acattttgcc tcgtggaccc aaaggttagca atctgaaaca tgaggagtac 100  
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgctt gggactccct cccacaaaaac tggctccgga tcagggaca 200  
ctaccaaacc aacagcagtc aaatcaggc tttccttctt taagtctgat 250  
accattaaca cagatgctca cactggggcc agatctgcat ctgttaatc 300  
ctgctgcagg aatgacacact ggtacccaga cccaccatt gaccctggga 350  
gggttgaatg tacaacagca actgcaccca catgtttac caattttgt 400  
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
aaatcttcac gagcctcatc atccattcct tggtcccgagg aggcattctg 500  
cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
agcaggagga gcaggtgtaa atcctgcccc ccaggaaacc ccagcaggcc 600  
gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650  
gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700  
agcaaatgga attcagtaag ctgtttcaaa tttttcaac taagctgcct 750  
cgaatttgggt gatacatgtg aatctttatc attgattata ttatggaata 800  
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850  
gaaaatattc ttgaaatttc agaaaatatg ttctatgttag agaatccaa 900  
ctttaaaaaa caataattca atggataaat ctgtcttga aatataacat 950  
tatgctgcct gnatgatatg catattaaaa catattgga aaactggaaa 1000  
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1050  
aaaaaaaaaaa aaaaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

Met	Arg	Ser	Thr	Ile	Leu	Leu	Phe	Cys	Leu	Leu	Gly	Ser	Thr	Arg
1				5				10				15		
Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
	20				25				30					
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Ser	Asn	
	35					40			45					
Gln	Val	Phe	Pro	Ser	Leu	Ser	Ile	Pro	Leu	Thr	Gln	Met	Leu	
	50				55		55		60					
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
	65				70				75					

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
80									85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
95									100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
110									115					120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
125									130					135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
140									145					150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
155									160					165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
170									175					180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
185									190					195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln	
200									205					

<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

```

ggagagaggc gcgcgggtga aaggcgatt gatgcagcct gcggcggcct 50
cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgacccccagg 150
cccccgccgc ctcccccgag cggctccgct gcctcctgct gtccttgctg 200
ctgcagctgc ccgcgcgcgtc gagcgcctct gagatccccca agggaaagca 250
aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
aatgttattc cgggtacacc tggatccca ggtcgggatg gattcaaagg 400
actacaagca gtgttcatgg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgtcttaag 550
agttttggtc agtggctcac ttccggctaaa atgcagaaaat gcatgctgtc 600
agcgttggta ttccacattc aatggagctg aatgttcagg acctcttccc 650

```

attgaagcta taattttattt ggaccaagga agccctgaaa tgaattcaac 700  
aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattt 750  
gtgctggatt agtggatgtt gctatctggg ttggcacttg ttcatcattac 800  
ccaaaaggag atgcttctac tggatggaat tcagttctc gcatcattat 850  
tgaagaacta cccaaataaa tgcttaatt ttcatggct acctctttt 900  
ttattatgcc ttgaaatggt tcacttaat gacatttaa ataagtttat 950  
gtatacatct gaatgaaaag caaagctaaa tatgttaca gaccaaagt 1000  
tgatttcaca ctgttttaa atcttagcatt attcatttt cttcaatcaa 1050  
aagtggtttc aatattttt ttagttgggtt agaatacttt cttcatagtc 1100  
acattctctc aacctataat ttgaaatatt gttgtggct tttgttttt 1150  
ctcttagtat agcattttt aaaaaatata aaagctacca atcttgcac 1200  
aatttgtaaa tgttaagaat ttttttata tctgttaaat aaaaattatt 1250  
tccaaca 1257

<210> 431

<211> 243

<212> PRT

<213> Homo Sapien

<400> 431

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1					5				10				15	
Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala						
								20		25			30	
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg
				35				40				45		
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala
				50				55				60		
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro
				65				70				75		
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys
				80				85				90		
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn
				95				100				105		
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu
				110				115				120		
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser
				125				130				135		

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg  
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu  
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln  
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser  
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp  
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp  
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu  
230 235 240

Leu Pro Lys

<210> 432  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Artificial Sequence

<400> 432  
aggacttgcc ctcagggaa 18

<210> 433  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 433  
cgcaggacag ttgtgaaaat a 21

<210> 434  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 434  
atgacgctcg tccaaaggcca c 21

<210> 435

<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 435  
cccacctgta ccaccatgt 19

<210> 436  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 436  
actccaggca ccatctgttc tccc 24

<210> 437  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 437  
aagggctggc attcaagtc 19

<210> 438  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 438  
tgacctggca aaggaagaa 19

<210> 439  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 439  
cagccaccct ccagtccaag g 21

<210> 440  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 440  
gggtcgtgtt ttggagaga 19

<210> 441  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 441  
ctggccctca gagcaccaat 20

<210> 442  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 442  
tcctccatca cttcccctag ctcca 25

<210> 443  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 443  
ctggcaggag ttcaaaggttcc aaga 24

<210> 444  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 444  
aaaggacacc gggatgtg 18

<210> 445  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 445  
agcgtacact ctctccaggc aaccag 26

<210> 446  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 446  
caattctgga tgaggtggta ga 22

<210> 447  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 447  
caggactgag cgcttgttta 20

<210> 448  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 448  
caaagcgcca agtaccggac c 21

<210> 449  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 449  
ccagacctca gccaggaa 18

<210> 450  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 450  
cccttagctga ccccttca 18

<210> 451  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 451  
tctgacaaggc agttttctga atc 23

<210> 452  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 452  
ctctccccct ccctttccct ttgttt 26

<210> 453  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 453  
ctctggtgcc cacagtga 18

<210> 454  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 454  
ccatgcctgc tcagccaaga a 21

<210> 455  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 455  
caggaaatct ggaaaacctac agt 23

<210> 456  
<211> 20  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456  
ccttgaaaag gacccagggtt 20

<210> 457

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 457  
atgagtcgca cctgctgttc cc 22

<210> 458

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 458  
tagcagctgc cttggta 18

<210> 459

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 459  
aacagcagggt gcgactcatc ta 22

<210> 460

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460  
tgctaggcga cgacacccag acc 23

<210> 461

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461  
tggacacgtg gcagtgg 18

<210> 462  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462  
tcatggtctc gtcccattc 19

<210> 463  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 463  
caccatttgt ttctctgtct ccccatc 27

<210> 464  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 464  
ccggcatcct tggagtag 18

<210> 465  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 465  
tccccattag cacaggagta 20

<210> 466  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 466

aggctttgc ctgtcctgct gct 23  
<210> 467  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 467  
gcccagagtc ccacttgt 18  
  
<210> 468  
<211> 19  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 468  
actgctccgc ctactacga 19  
  
<210> 469  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 469  
aggcatcctc gccgtctca 20  
  
<210> 470  
<211> 19  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 470  
aaggccaagg tgagtccat 19  
  
<210> 471  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 471  
cgagtgttg cgaaacctaa 20  
  
<210> 472

<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 472  
tcagggtcta catcagcctc ctgc 24

<210> 473  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 473  
aaggccaagg tgagtccat 19

<210> 474  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 474  
cctactgagg agccctatgc 20

<210> 475  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 475  
tccaggtgga ccccacttca gg 22

<210> 476  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 476  
gggaggctta taggccccat ctgg 24

<210> 477  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50